

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OH nucleic - nucleic search, using sw model
Run on: March 26, 2001, 12:45:42 : Search time 15045.6 Seconds
(without alignments)
5398.140 Million cell updates/sec

Title: ur-09-410-835-4

Perfect score: 5925

Sequence: 1 cccattttagcactcca.....tttttagatgacacagctt 5925

Scoring table: OLIGO_NUC
Gapop 60.0, Deapct 60.0

Searched: 118133 seqs, 6853842396 residues

Word size: 15

Total number of hits satisfying chosen parameters: 118785

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database:

GenBank:
1: gb_dna1
2: gb_dna2
3: gb_dna3
4: gb_dna4
5: gb_dna5
6: gb_dna6
7: gb_dna7
8: gb_dna8
9: gb_dna9
10: gb_dna10
11: gb_dna11
12: gb_dna12
13: gb_dna13
14: gb_dna14
15: gb_dna15
16: gb_dna16
17: gb_dna17
18: gb_dna18
19: gb_dna19
20: gb_dna20
21: gb_dna21

Tue Mar 27 09:32:16 2001

ur-09-410-835-4.ollg.rge

Page 3

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Query	Match length	DB ID	Description
1	5925 100.0	5925 2	AX010124	Sequence
2	5925 100.0	5925 61	A76409	X700379 H. pylori CA
3	5925 100.0	5925 61	A76409	A76409 Sequence 4
4	5925 100.0	5925 61	A76409	A76409 Sequence 4
5	5925 100.0	5925 61	A76409	A76409 Sequence 4
6	5925 100.0	5925 61	A76409	A76409 Sequence 4
7	5925 100.0	5925 61	A76409	A76409 Sequence 4
8	5925 100.0	5925 61	A76409	A76409 Sequence 4
9	5925 100.0	5925 61	A76409	A76409 Sequence 4
10	5925 100.0	5925 61	A76409	A76409 Sequence 4
11	5925 100.0	5925 61	A76409	A76409 Sequence 4
12	5925 100.0	5925 61	A76409	A76409 Sequence 4
13	5925 100.0	5925 61	A76409	A76409 Sequence 4
14	5925 100.0	5925 61	A76409	A76409 Sequence 4
15	5925 100.0	5925 61	A76409	A76409 Sequence 4
16	5925 100.0	5925 61	A76409	A76409 Sequence 4
17	5925 100.0	5925 61	A76409	A76409 Sequence 4
18	5925 100.0	5925 61	A76409	A76409 Sequence 4
19	5925 100.0	5925 61	A76409	A76409 Sequence 4
20	5925 100.0	5925 61	A76409	A76409 Sequence 4
21	5925 100.0	5925 61	A76409	A76409 Sequence 4
22	5925 100.0	5925 61	A76409	A76409 Sequence 4
23	5925 100.0	5925 61	A76409	A76409 Sequence 4
24	5925 100.0	5925 61	A76409	A76409 Sequence 4
25	5925 100.0	5925 61	A76409	A76409 Sequence 4
26	5925 100.0	5925 61	A76409	A76409 Sequence 4
27	5925 100.0	5925 61	A76409	A76409 Sequence 4
28	5925 100.0	5925 61	A76409	A76409 Sequence 4
29	5925 100.0	5925 61	A76409	A76409 Sequence 4
30	5925 100.0	5925 61	A76409	A76409 Sequence 4
31	5925 100.0	5925 61	A76409	A76409 Sequence 4
32	5925 100.0	5925 61	A76409	A76409 Sequence 4
33	5925 100.0	5925 61	A76409	A76409 Sequence 4
34	5925 100.0	5925 61	A76409	A76409 Sequence 4
35	5925 100.0	5925 61	A76409	A76409 Sequence 4
36	5925 100.0	5925 61	A76409	A76409 Sequence 4
37	5925 100.0	5925 61	A76409	A76409 Sequence 4
38	5925 100.0	5925 61	A76409	A76409 Sequence 4
39	5925 100.0	5925 61	A76409	A76409 Sequence 4
40	5925 100.0	5925 61	A76409	A76409 Sequence 4
41	5925 100.0	5925 61	A76409	A76409 Sequence 4
42	5925 100.0	5925 61	A76409	A76409 Sequence 4
43	5925 100.0	5925 61	A76409	A76409 Sequence 4
44	5925 100.0	5925 61	A76409	A76409 Sequence 4
45	5925 100.0	5925 61	A76409	A76409 Sequence 4
46	5925 100.0	5925 61	A76409	A76409 Sequence 4
47	5925 100.0	5925 61	A76409	A76409 Sequence 4
48	5925 100.0	5925 61	A76409	A76409 Sequence 4
49	5925 100.0	5925 61	A76409	A76409 Sequence 4
50	5925 100.0	5925 61	A76409	A76409 Sequence 4
51	5925 100.0	5925 61	A76409	A76409 Sequence 4
52	5925 100.0	5925 61	A76409	A76409 Sequence 4
53	5925 100.0	5925 61	A76409	A76409 Sequence 4
54	5925 100.0	5925 61	A76409	A76409 Sequence 4
55	5925 100.0	5925 61	A76409	A76409 Sequence 4
56	5925 100.0	5925 61	A76409	A76409 Sequence 4
57	5925 100.0	5925 61	A76409	A76409 Sequence 4
58	5925 100.0	5925 61	A76409	A76409 Sequence 4
59	5925 100.0	5925 61	A76409	A76409 Sequence 4
60	5925 100.0	5925 61	A76409	A76409 Sequence 4
61	5925 100.0	5925 61	A76409	A76409 Sequence 4
62	5925 100.0	5925 61	A76409	A76409 Sequence 4
63	5925 100.0	5925 61	A76409	A76409 Sequence 4
64	5925 100.0	5925 61	A76409	A76409 Sequence 4
65	5925 100.0	5925 61	A76409	A76409 Sequence 4
66	5925 100.0	5925 61	A76409	A76409 Sequence 4
67	5925 100.0	5925 61	A76409	A76409 Sequence 4
68	5925 100.0	5925 61	A76409	A76409 Sequence 4
69	5925 100.0	5925 61	A76409	A76409 Sequence 4
70	5925 100.0	5925 61	A76409	A76409 Sequence 4
71	5925 100.0	5925 61	A76409	A76409 Sequence 4
72	5925 100.0	5925 61	A76409	A76409 Sequence 4
73	5925 100.0	5925 61	A76409	A76409 Sequence 4
74	5925 100.0	5925 61	A76409	A76409 Sequence 4
75	5925 100.0	5925 61	A76409	A76409 Sequence 4
76	5925 100.0	5925 61	A76409	A76409 Sequence 4
77	5925 100.0	5925 61	A76409	A76409 Sequence 4
78	5925 100.0	5925 61	A76409	A76409 Sequence 4
79	5925 100.0	5925 61	A76409	A76409 Sequence 4
80	5925 100.0	5925 61	A76409	A76409 Sequence 4
81	5925 100.0	5925 61	A76409	A76409 Sequence 4
82	5925 100.0	5925 61	A76409	A76409 Sequence 4
83	5925 100.0	5925 61	A76409	A76409 Sequence 4
84	5925 100.0	5925 61	A76409	A76409 Sequence 4
85	5925 100.0	5925 61	A76409	A76409 Sequence 4

length of match

22: em_dna1
23: em_dna2
24: em_dna3
25: em_dna4
26: em_dna5
27: em_dna6
28: em_dna7
29: em_dna8
30: em_dna9
31: em_dna10
32: em_dna11
33: em_dna12
34: em_dna13
35: em_dna14
36: em_dna15
37: em_dna16
38: em_dna17
39: em_dna18
40: em_dna19
41: em_dna20
42: em_dna21
43: em_dna22
44: em_dna23
45: em_dna24
46: em_dna25
47: em_dna26
48: em_dna27
49: em_dna28
50: em_dna29
51: em_dna30
52: em_dna31
53: em_dna32
54: em_dna33
55: em_dna34
56: em_dna35
57: em_dna36
58: em_dna37
59: em_dna38
60: em_dna39
61: em_dna40
62: em_dna41
63: em_dna42
64: em_dna43
65: em_dna44
66: em_dna45
67: em_dna46
68: em_dna47
69: em_dna48
70: em_dna49
71: em_dna50
72: em_dna51

Tue Mar 27 09:32:16 2001

ur-09-410-835-4.ollg.rge

Page 4

29	179	3.0	449	2	HPY269879	AJ269879 Helicobac
30	179	3.0	449	2	HPY269882	AJ269882 Helicobac
31	175	3.0	449	2	HPY239691	AJ239691 Helicobac
32	175	3.0	449	2	HPY269888	AJ269888 Helicobac
33	164	3.0	449	2	HPY269893	AJ269893 Helicobac
34	164	3.0	449	2	HPY269895	AJ269895 Helicobac
35	167	2.8	672	2	AE289438	AE289438 Helicobac
36	166	2.8	10781	1	AE289433	AE289433 Helicobac
37	158	2.7	291	2	AE289405	AE289405 Helicobac
38	158	2.7	291	2	AE289405	AE289405 Helicobac
39	158	2.7	291	2	AE289405	AE289405 Helicobac
40	157	2.6	291	2	AE289405	AE289405 Helicobac
41	157	2.6	291	2	AE289405	AE289405 Helicobac
42	156	2.6	449	2	HPY269889	AJ269889 Helicobac
43	156	2.6	449	2	HPY269889	AJ269889 Helicobac
44	154	2.6	291	2	AE289405	AE289405 Helicobac
45	153	2.6	291	2	AE289405	AE289405 Helicobac
46	152	2.6	1323	1	AE222809	AE222809 Helicobac
47	149	2.5	413	2	HPY239692	AJ239692 Helicobac
48	149	2.5	413	2	HPY239692	AJ239692 Helicobac
49	144	2.4	291	2	AE289405	AE289405 Helicobac
50	140	2.4	220	1	AP198482	AP198482 Helicobac
51	140	2.4	243	2	HPY239736	AJ239736 Helicobac
52	140	2.4	281	1	AP198482	AP198482 Helicobac
53	140	2.4	281	1	AP198482	AP198482 Helicobac
54	140	2.4	413	2	HPY239690	AJ239690 Helicobac
55	138	2.3	449	2	HPY269884	AJ269884 Helicobac
56	138	2.3	344	1	AE201397	AE201397 Helicobac
57	138	2.3	344	1	AE201397	AE201397 Helicobac
58	138	2.3	344	1	AE201397	AE201397 Helicobac
59	137	2.3	220	1	AP198474	AP198474 Helicobac
60	137	2.3	243	2	HPY239732	AJ239732 Helicobac
61	137	2.3	243	2	HPY239732	AJ239732 Helicobac
62	137	2.3	243	2	HPY239732	AJ239732 Helicobac
63	137	2.3	243	2	HPY239732	AJ239732 Helicobac
64	137	2.3	243	2	HPY239732	AJ239732 Helicobac
65	137	2.3	243	2	HPY239732	AJ239732 Helicobac
66	137	2.3	243	2	HPY239732	AJ239732 Helicobac
67	137	2.3	243	2	HPY239732	AJ239732 Helicobac
68	137	2.3	243	2	HPY239732	AJ239732 Helicobac
69	137	2.3	243	2	HPY239732	AJ239732 Helicobac
70	136	2.3	243	2	HPY239732	AJ239732 Helicobac
71	136	2.3	243	2	HPY239732	AJ239732 Helicobac
72	136	2.3	243	2	HPY239732	AJ239732 Helicobac
73	136	2.3	243	2	HPY239732	AJ239732 Helicobac
74	136	2.3	243	2	HPY239732	AJ239732 Helicobac
75	136	2.3	243	2	HPY239732	AJ239732 Helicobac
76	136	2.3	243	2	HPY239732	AJ239732 Helicobac
77	136	2.3	243	2	HPY239732	AJ239732 Helicobac
78	136	2.3	243	2	HPY239732	AJ239732 Helicobac
79	136	2.3	243	2	HPY239732	AJ239732 Helicobac
80	136	2.3	243	2	HPY239732	AJ239732 Helicobac
81	136	2.3	243	2	HPY239732	AJ239732 Helicobac
82	136	2.3	243	2	HPY239732	AJ239732 Helicobac
83	136	2.3	243	2	HPY239732	AJ239732 Helicobac
84	136	2.3	243	2	HPY239732	AJ239732 Helicobac
85	136	2.3	243	2	HPY239732	AJ239732 Helicobac

80	118	2.0	291	2	AF289407
81	118	2.0	291	2	AF289407
82	116	2.0	540	2	AF289417
83	116	2.0	540	2	AF289417
84	115	2.0	567	2	AF289450
85	115	2.0	567	2	AF289457
86	115	2.0	567	2	AF289457
87	111	1.9	291	2	AF289416
88	111	1.9	291	2	AF289416
89	110	1.9	291	2	AF289416
90	109	1.8	291	2	AF289416
91	108	1.8	464	2	AF289416
92	108	1.8	464	2	AF289416
93	108	1.8	464	2	AF289416
94	107	1.8	291	2	AF289416
95	107	1.8	291	2	AF289416
96	107	1.8	291	2	AF289416
97	104	1.8	566	2	AF289416
98	101	1.7	567	2	AF289416
99	101	1.7	567	2	AF289416
100	101	1.7	567	2	AF289416
101	100	1.7	291	2	AF289416
102	100	1.7	291	2	AF289416
103	100	1.7	291	2	AF289416
104	100	1.7	291	2	AF289416
105	100	1.7	291	2	AF289416
106	100	1.7	291	2	AF289416
107	100	1.7	291	2	AF289416
108	100	1.7	291	2	AF289416
109	100	1.7	291	2	AF289416
110	100	1.7	291	2	AF289416
111	98	1.7	291	2	AF289416
112	97	1.6	489	2	AF289416
113	96	1.6	489	2	AF289416
114	96	1.6	489	2	AF289416
115	96	1.6	1000	1	AF190993
116	94	1.6	940	1	AF190994
117	94	1.6	3522	1	AF202972
118	92	1.6	243	2	AF202972
119	92	1.6	243	2	AF202972
120	89	1.5	291	2	AF289412
121	89	1.5	291	2	AF289412
122	89	1.5	291	2	AF289412
123	89	1.5	291	2	AF289412
124	89	1.5	291	2	AF289412
125	88	1.5	678	2	AF289412
126	88	1.5	10351	1	AE000560
127	87	1.5	291	2	AF289412
128	86	1.5	243	2	AF289412
129	86	1.5	243	2	AF289412
130	86	1.5	243	2	AF289412

182	60	1.0	291	2	AF289393
183	60	1.0	291	2	AF289397
184	58	1.0	464	2	AF289397
185	58	1.0	464	2	AF289397
186	57	1.0	387	1	AF191003
187	57	1.0	444	1	AF191003
188	57	1.0	513	2	AF289454
189	57	1.0	513	2	AF289454
190	56	0.9	287	1	AF202219
191	56	0.9	287	1	AF202219
192	56	0.9	287	1	AF202219
193	56	0.9	287	1	AF202219
194	56	0.9	452	2	AF289454
195	56	0.9	452	2	AF289454
196	55	0.9	444	2	AF289454
197	55	0.9	444	2	AF289454
198	55	0.9	444	2	AF289454
199	55	0.9	444	2	AF289454
200	55	0.9	444	2	AF289454
201	53	0.9	243	2	AF289412
202	53	0.9	243	2	AF289412
203	52	0.9	464	2	AF289454
204	52	0.9	464	2	AF289454
205	52	0.9	464	2	AF289454
206	49	0.8	387	1	AF289454
207	49	0.8	387	1	AF289454
208	49	0.8	413	2	AF289454
209	49	0.8	413	2	AF289454
210	49	0.8	413	2	AF289454
211	49	0.8	413	2	AF289454
212	49	0.8	464	2	AF289454
213	49	0.8	464	2	AF289454
214	49	0.8	464	2	AF289454
215	49	0.8	464	2	AF289454
216	46	0.8	291	2	AF289394
217	46	0.8	464	2	AF289394
218	46	0.8	464	2	AF289394
219	46	0.8	464	2	AF289394
220	46	0.8	464	2	AF289394
221	46	0.8	464	2	AF289394
222	46	0.8	464	2	AF289394
223	46	0.8	464	2	AF289394
224	46	0.8	464	2	AF289394
225	46	0.8	464	2	AF289394
226	46	0.8	464	2	AF289394
227	46	0.8	464	2	AF289394
228	46	0.8	464	2	AF289394
229	46	0.8	464	2	AF289394
230	46	0.8	464	2	AF289394
231	46	0.8	464	2	AF289394
232	46	0.8	464	2	AF289394

111	86	1.5	244	2	AF289454
112	86	1.5	244	2	AF289454
113	86	1.5	244	2	AF289454
114	86	1.5	244	2	AF289454
115	86	1.5	244	2	AF289454
116	86	1.5	244	2	AF289454
117	86	1.5	244	2	AF289454
118	86	1.5	244	2	AF289454
119	86	1.5	244	2	AF289454
120	86	1.5	244	2	AF289454
121	86	1.5	244	2	AF289454
122	86	1.5	244	2	AF289454
123	86	1.5	244	2	AF289454
124	86	1.5	244	2	AF289454
125	86	1.5	244	2	AF289454
126	86	1.5	244	2	AF289454
127	86	1.5	244	2	AF289454
128	86	1.5	244	2	AF289454
129	86	1.5	244	2	AF289454
130	86	1.5	244	2	AF289454

233	40	-0.7	4751	1	AF289450
234	39	0.7	626	1	AF289450
235	39	0.7	626	1	AF289450
236	39	0.7	626	1	AF289450
237	38	0.6	413	2	AF289450
238	38	0.6	464	2	AF289450
239	38	0.6	464	2	AF289450
240	38	0.6	464	2	AF289450
241	38	0.6	464	2	AF289450
242	38	0.6	464	2	AF289450
243	38	0.6	464	2	AF289450
244	37	0.6	413	2	AF289450
245	37	0.6	413	2	AF289450
246	37	0.6	413	2	AF289450
247	37	0.6	413	2	AF289450
248	37	0.6	413	2	AF289450
249	35	0.6	291	2	AF289394
250	35	0.6	291	2	AF289394
251	35	0.6	291	2	AF289394
252	35	0.6	291	2	AF289394
253	35	0.6	291	2	AF289394
254	35	0.6	291	2	AF289394
255	35	0.6	291	2	AF289394
256	35	0.6	291	2	AF289394
257	35	0.6	291	2	AF289394
258	35	0.6	291	2	AF289394
259	35	0.6	291	2	AF289394
260	35	0.6	291	2	AF289394
261	35	0.6	291	2	AF289394
262	35	0.6	291	2	AF289394
263	35	0.6	291	2	AF289394
264	35	0.6	291	2	AF289394
265	35	0.6	291	2	AF289394
266	35	0.6	291	2	AF289394
267	35	0.6	291	2	AF289394
268	35	0.6	291	2	AF289394
269	35	0.6	291	2	AF289394
270	35	0.6	291	2	AF289394
271	35	0.6	291	2	AF289394
272	35	0.6	291	2	AF289394
273	35	0.6	291	2	AF289394
274	35	0.6	291	2	AF289394
275	35	0.6	291	2	AF289394
276	35	0.6	291	2	AF289394
277	35	0.6	291	2	AF289394
278	35	0.6	291	2	AF289394
279	35	0.6	291	2	AF289394
280	35	0.6	291	2	AF289394
281	35	0.6	291	2	AF289394
282	35	0.6	291	2	AF289394
283	35	0.6	291	2	AF289394
284	35	0.6	291	2	AF289394
285	35	0.6	291	2	AF289394
286	35	0.6	291	2	AF289394
287	35	0.6	291	2	AF289394
288	35	0.6	291	2	AF289394
289	35	0.6	291	2	AF289394
290	35	0.6	291	2	AF289394
291	35	0.6	291	2	AF289394
292	35	0.6	291	2	AF289394
293	35	0.6	291	2	AF289394
294	35	0.6	291	2	AF289394
295	35	0.6	291	2	AF289394
296	35	0.6	291	2	AF289394
297	35	0.6	291	2	AF289394
298	35	0.6	291	2	AF289394
299	35	0.6	291	2	AF289394
300	35	0.6	291	2	AF289394


```

RESULT# 4
LOCUS AF282853          DNA                      BCT              16-AUG-2000
DEFINITION Helicobacter pylori cagI pathogenicity island, complete sequence.
VERSION      Hel282853.1
AUTHORS      Hel282853.1
REMARKS
SOURCE       GenBank
ORGANISM     Helicobacter pylori; epsilon subdivision; Helicobacter group;
             Helicobacter pylori;
             Helicobacter pylori;
             Helicobacter pylori;
REFERENCE    1 [base 1 to 20239] Covacci,A., and Rappapoli,R. Tyrosine-phosphorylated protein: Trojan horses for the
              gastric epithelium?
              Exp. Med. 191 (4), 587-592 (2000)
JOURNAL MEDLINE 2 [base 1 to 20239] Covacci,A. and Rappapoli,R.
              Tyrosine-phosphorylated protein: Trojan horses for the
              gastric epithelium?
              J. Exp. Med. 191 (4), 587-592 (2000)
REFERENCE    3 [base 1 to 20239] D'Amico,A., Lange,C. and Covacci,A.
              Direct submission
              Submitted (06-JUN-1996) Molecular Biology, Chiron-Biotec, via
              Fiorentina I, Siena, SI 53100, Italy
              Firenze,I.
              Covacci,A., Rappapoli,R. and Covacci,A.
              Direct Submission
              Submitted (17-MAR-2000) Molecular Biology, Chiron-Biotec, via
              Fiorentina I, Siena, SI 53100, Italy
              On Jun 30 2000 this sequence version replaced gi|1732460.
COMMENT      Location/Qualifiers
FEATURES             1..20239
                   /organism="Helicobacter pylori";
                   /project="CH11783";
                   /db_xref="taxon:210";
                   /note="Type I specific and disease-associated virulence
factor gene: partial sequence of cag pathogenicity island"

```

[illegible]

Tue Mar 27 09:32:16 2001

us-09-410-835-4.01lg.rge

Page 51

Tue Mar 27 09:32:16 2001

us-09-410-B35-4.011g.rge

Page 52

[illegible][illegible]

	LOCUS	HPIY91868	413 bp	DNA	BCT	30-JUN-1999
	DEFINITION	Helicobacter pylori partial caga gene, strain NCTC11613.				
	ACCESSION	AJ239688				
	VERSION	AJ239688.1	GI:4467694			
	KEYWORDS	caga gene,				
	SOURCE	Helicobacter pylori.				
	ORGANISM	Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;				
	REFERENCE	1. (bases 1 to 413)				
	AUTHORS	Achtmann,M.; Mama,T.J., Berg,D.E., Ito,Y., Korelli,G., Pan,E.J., Stehnbach,S., Thompson,A.N., Van Der Ende,A., and Van Duyn,L.J. Microbiological and clinical significance within helicobacter pylori from dyspeptic patients and healthy controls				
	JOURNAL	Nat. Microbiol. 3(3), 459-470 (1999)				
	MEDLINE	99255683				
	REFERENCE SOURCE	2. (bases 1 to 413)				
	TITLE	Direct Submission				
	JOURNAL	Submitted (32-FEB-1999) Suerbaum S., Medical Microbiology, RHM-Universalreizeit Bochum, Universitaetssatzung 150, D-44801 Bochum, GERMANY				
FEATURES	source	Location/Qualifiers				
		/organism=Helicobacter pylori*				
		/db_xref=taxon:210*				
		/country=Australia*				
	gene	1..413				
	CDS	/gene=cagA*				
		/gene=cagN*				
		/gene=cagX*				
		/codon_start=1				
		/transl_table=1				
		/protein_id=CAB37759.1*				
		/date_created='1999-1'				
		/db_xref=GI:4467695*				
		/translation='EATFNGQDFIINNLAVALFEVONAVASTDPKPYVDNDDEBRC' AFDLSLSELRISNRSLNSGSDLVHIMDLIDVESSTSFSPNFALCF' AGTSSPLSRPSFTSGTSFESRLIRPQ*				
	ORIGIN	153 ac				
	BASE COUNT	153 a c g t				
		67 g 109 t				
	Query Match	6.0% score 353; DB 2; Length 413:				
	Best Local Similarity	99.8%; Prnd. No. 1.5e-156;				
	Matches 403	Conservative 0; Mismatched 1; Indels 0; Gaps 0;				
Oy	580	tttaacccgcaccatttatacctaacgaagtcatgactgttcataagtgataaatcg 639				
db	10	tTTAAccCGCaCCAtTAATAACAACCACTGAAGCACCTTCGTAAAGCATTAACGC 69				

Tue Mar 27 09:32:16 2001

US-09-410-835-4.011g.rge

Page 63

```

source
1. 413
/organism="Heliobacter pylori"
/db_xref="taxon 210"
/county="USA, Alaska"
1. 413gbp
<100>413bp
/gene="cagA"
/codon_start=1
/translation="EALNPOQFNNLQVAFLEKYNLVASTDPQKPYDKNDNRG
/translation="GI 4457689"
/translation="EALNPOQFNNLQVAFLEKYNLVASTDPQKPYDKNDNRG
ORIGIN
BASE COUNT      149 A      84 C      69 G      112 T
ORIGIN
Query Match          5.3% Score 316: DB 3: Length 413:
Beat Local Similarity 99.7%: Pval: 0.61e-119:
Matches 366: Conservative 0: Mismatches 1: Indels 0: Gaps 0:
Oy 571 gaagggattatgaccgcgcgataatcacaataacgttcgaagcttcgaagctt 640
|||
Db 1 gaaccgcttttaacccgcacgattttatcaataatttcacgacgtctttttaaatt 60
Oy 613 gataaacgtcttcgctcttcgataatgataacaaacatctgataaacgaataag 650
|||
Db 61 gatatacgtcttccttcacatccatccatcaaaacacatcttcataacgaatcag 120
Oy 691 gataacgagcagatcttcgaaggaattctgcgaatttaaggaagaatcacaataag 750
|||
Db 121 gatatacgcgaacacgttttaacatcttcacatttaaggaacaaatccatcaaaac 180
Oy 751 atcaaaaactccacaaaagaatcagatcttcttcagacttcacataaagcagaat 810
|||
Db 181 atccaaaactccacaaaagaatcagatcttcttcagacttcacataaagcagaat 240
Oy 811 ttaactcaaaaagcacaatcatttgaagataactccacaaaagcgtcttcagaatt 870
|||
Db 241 ttaactcaaaaagcacaatcatttgaagataactccacaaaagcgtcttcagaatt 300
Oy 871 gggagatcagatccgcgaattcttcacgaattcggagctcccaaaaagatccgctcaa 930
|||
Db 301 cggacatccacgttaccgaatttcaaaatctgcacatccatccatccatccatccatca 360
Oy 931 atcaacaa 937
|||||||

```

[illegible]

Tue Mar 27 09:32:16 2001

us-09-410-835-4.01lg.rge

Page 64

Db	1209	AGCTCGATGATAGGCGATGAGCGATGCGACCTTTGAGCGGATCTCCGACATTTAAAG	1368
Oy	730	GAAATATCTCGCTAAAGAGGATCAATATCTCGCGGAAATGATGATTTTTCGAGC	789
Db	1269	GAAATATCTCGCTAAAGCGACATTAATCTGTCGCAAAAGATGCTGTTTTCGAC	1328
Oy	732	TTTTCATCATGAGGATGATCTTAAAGCGGATGCGATGCGATGCTGATG	835
Db	1329	TTTTCATCATGAGCGATGATTTTAAATCGAATGCGATGCGATGCTGATG	1374
RESULT	19		
LOCUS	AF247651	3540 bp	DNA
DEFINITION	Helicobacter pylori cytochrome-associated protein cagA (cagA) gene,	BC7	13-APR-2000
ACCESSION	AF247651	cds.	
VERSION	AF247651.1	GI:7547015	
KEYWORDS	Helicobacter pylori; Helicobacter pylori; Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group; Helicobacter		
ORIGIN	Helicobacter strain 1 to 3540)		
REFERENCE	1. Ushigoe M, et al. (1999) The cagA gene of Helicobacter pylori (SS1 strain)		
AUTHORS	Ushigoe M, et al.		
JOURNAL	Journal of Clinical Microbiology		
TITLE	Direct Submission		
REFERENCE	2. Baaga 1 to 3540)		
COMMENT	Submitted (21-APR-2000) Dept. of Diarrhea Disease, Institute of Epidemiology and Microbiology, Chinese Academy of Preventive Medicine, Location/Qualifiers		
FEATURES	1. 3540		
SOURCE			

```

      /db.xref="taxon:210"
      /clone="prssi"
      1..3540
      /gene="CsgA"
      1..3540
      CDS
      1..3540
      /gene="CsgA"
      /catalytic_site="1"
      /product="cytoxin-associated protein CsgA"
      /protein_id="AF0395.1"
      /translation="MTGKLTGKQPTGTAENPQGTAAENPQVLAENLADNVAAYDQPK
      PTKNDKIDNRGAFGCSGLAEKSNKIAKPTKKNKYSDFINISDPLDQV

```



```

JOURNAL      Submitted (29-SEP-1999) Molecular Microbiology, Washington
              University Health Center, 4566 Scott Ave., St. Louis, MO 63110.
EXFEATURES
source       USA
            location/Qualifiers
            1 787
            /organism="Helicobacter pylori"
            /strain="india75A"
            /map="between HP0547 and HP0549 in 26695 genome"
            /country="India, Calcutta"
            /note="Isolated from a gastric ulcer patient; polymorphic
            region at right end of the cas pathogenicity island; type
            type IIIa motif presented in Genbank Accession Number
            AF196662"
            31. 430
            /note="similar to Helicobacter pylori insertion sequence
            element described in Genbank Accession Number U93937"
            66. 313
            /organism="Helicobacter pylori"
            /strain="india75A"
            /map="between HP0547 and HP0549 in 26695 genome"
            /insertion_seq="mini5605"
            /country="India, Calcutta"
            /note="Isolated from a gastric ulcer patient; polymorphic
            region at right end of the cas pathogenicity island; type
            IIIb motif; similar to type IIIa motif"
            495. 744
            /note="this sequence differs from type I strains such as
            this location"
            431. 787
            /note="this sequence contains a putative helicase gene at
            this location(353. >787)"
            /gene="glt"
            /note="complement(755. >787)"
            /gene="glt"
            /note="similar to Helicobacter pylori strain 26695
            glutamate isomerase HP0549"
            /transl_table=1
            /product="glutamate isomerase"
            /protein_id="AC014466.1"
            /translation="EQQKFKFKAK"
            /note="ORIGIN"
            137 c 173 g 245 t
            332 a
BASE COUNT
ORIGIN
Query Match      3.14; Score 181; DB 1; Length 787;
Query Local Similarity 99.64; Pred. No. 1e-74;

```

Tue Mar 27 09:32:16 2001

us-09-410-835-4.01lg.rge

Page 103

us-09-410-835-4.0119.rge

Page 104

Tue Mar 27 09:32:16 2001

us-09-410-835-4.0119.rge

Page 104

FEATURES	source
LOCUS	HPY2698B3
DEFINITION	Helicobacter pylori partial caga gene for Caga protein, isolate
ACCESSION	AF269881
VERSION	AJ269881.1
KEYWORDS	caga gene; Caga protein; Helicobacter pylori
ORGANISM	Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group; Helicobacter.
REFERENCE	1. (bases 1 to 449)
TITLE	Duplicate variants of Helicobacter pylori caga are associated with
JOURNAL	var. subtypes
REFERENCE	J. Clin. Microbiol. 37 (7), 2306-2311 (1999)
AUTHORS	Van Doorn L.J.
TITLE	Direct Subtyping
JOURNAL	Submitted (13-SEP-1999 van Doorn L.J., Molecular Biology, Delta
FEATURES	Microbiology, N. de Graafsvogel, Delft, 2029 AB).
source	1. .449

Tue Mar 27 09:32:16 2001

us-09-410-835-4.011g.rge

Page 111

Tue Mar 27 09:32:16 2001

US-09-410-835-4.011g.rge

Page 112

gene
9895..10716
CDS
ORIGIN
BASE COUNT 3585 A 1918 C 2165 G 3113 T

Query Match 2.8% Score 166; DB 1; Length 10781;
Best Local Similarity 99.5%; Pred. No. 1,2e-67;
Matches 216; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2628 taaactcttggaattccaaatgcaaaatgcaagcttcgaagcaagaaac 2637
DB 2532 taaactcttggaattccaaatgcaaaatgcaagcttcgaagcaagaaac 2531
QY 2688 actaaagcccttaagcttggaattccaaatgcaagcttcgaagcaagaaac 2747
DB 2592 actaaagcccttaagcttggaattccaaatgcaagcttcgaagcaagaaac 2641
QY 2748 agttaaagcccttaagcttggaattccaaatgcaagcttcgaagcaagaaac 2807
DB 2642 acttaaagcccttaagcttggaattccaaatgcaagcttcgaagcaagaaac 2701
QY 2808 caagcttggaattccaaatgcaagcttcgaagcaagaaac 2844
DB 2702 caagcttggaattccaaatgcaagcttcgaagcaagaaac 2738

RESULT 37
AF289406 291 bp DNA BCT 02-SEP-2000
LOCUS Helicobacter pylori isolate CR9 cytotoxin associated protein A
DEFINITION (caga) gene, partial cds.
ACCESSION AF289406.1 GI:9964166
VERSION AF289406.1 GI:9964166
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori

DB 138 atttttcaagcttggaattccaaatgcaaaatgcaagcttcgaagcaagaaac 197
QY 948 cgaatcttggaattccaaatgcaaaatgcaagcttcgaagcaagaaac 985
DB 198 cgaatcttggaattccaaatgcaaaatgcaagcttcgaagcaagaaac 235

RESULT 38
AF289417 291 bp DNA BCT 02-SEP-2000
LOCUS Helicobacter pylori isolate CR42 cytotoxin associated protein A
DEFINITION (caga) gene, partial cds.
ACCESSION AF289417.1 GI:9964168
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori

REFERENCE
AUTHORS Ouchiallin, A., Urdaci, M., Sierra, R., Munoz, N.,
TITLES Composition and gene expression of the cag pathogenicity island in
Helicobacter pylori strains isolated from gastric carcinoma and
gastritis patients in Costa Rica
JOURNAL Unpublished
PAGES 1 to 291
COUNTRY Costa Rica
SUBMITTED (26-JUL-2000) Laboratory of Bacteriology, University of
Bordeaux 2, 146 rue Leo Saignat, Bordeaux 33076, France
FEATURES
SOURCE
ORGANISM Helicobacter pylori
REFERENCE AF289417 291 bp DNA BCT 02-SEP-2000
LOCUS Helicobacter pylori isolate CR42
DEFINITION (caga) gene, partial cds.
ACCESSION AF289417.1 GI:9964168
VERSION AF289417.1 GI:9964168
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori

RESULT 39
AF289417 291 bp DNA BCT 02-SEP-2000
LOCUS Helicobacter pylori isolate CR42
DEFINITION (caga) gene, partial cds.
ACCESSION AF289417.1 GI:9964168
VERSION AF289417.1 GI:9964168
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori

REFERENCE
AUTHORS Ouchiallin, A., Urdaci, M., Sierra, R., Munoz, N.,
TITLES Composition and gene expression of the cag pathogenicity island in
Helicobacter pylori strains isolated from gastric carcinoma and
gastritis patients in Costa Rica
JOURNAL Unpublished
PAGES 1 to 291
COUNTRY Costa Rica
SUBMITTED (26-JUL-2000) Laboratory of Bacteriology, University of
Bordeaux 2, 146 rue Leo Saignat, Bordeaux 33076, France
FEATURES
SOURCE
ORGANISM Helicobacter pylori
REFERENCE AF289417 291 bp DNA BCT 02-SEP-2000
LOCUS Helicobacter pylori isolate CR42
DEFINITION (caga) gene, partial cds.
ACCESSION AF289417.1 GI:9964168
VERSION AF289417.1 GI:9964168
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori

REFERENCE
AUTHORS Ouchiallin, A., Urdaci, M., Sierra, R., Munoz, N.,
TITLES Composition and gene expression of the cag pathogenicity island in
Helicobacter pylori strains isolated from gastric carcinoma and
gastritis patients in Costa Rica
JOURNAL Unpublished
PAGES 1 to 291
COUNTRY Costa Rica
SUBMITTED (26-JUL-2000) Laboratory of Bacteriology, University of
Bordeaux 2, 146 rue Leo Saignat, Bordeaux 33076, France
FEATURES
SOURCE
ORGANISM Helicobacter pylori
REFERENCE AF289417 291 bp DNA BCT 02-SEP-2000
LOCUS Helicobacter pylori isolate CR42
DEFINITION (caga) gene, partial cds.
ACCESSION AF289417.1 GI:9964168
VERSION AF289417.1 GI:9964168
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori

Query Match 2.7% Score 158; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 9.4e-64;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 828 tccatcttggaattccaaatgcaaaatgcaagcttcgaagcaagaaac 887
DB 78 tccatcttggaattccaaatgcaaaatgcaagcttcgaagcaagaaac 137
QY 888 attttcaagcttggaattccaaatgcaaaatgcaagcttcgaagcaagaaac 947
DB 138 attttcaagcttggaattccaaatgcaaaatgcaagcttcgaagcaagaaac 197
QY 948 cgaatcttggaattccaaatgcaaaatgcaagcttcgaagcaagaaac 985
DB 198 cgaatcttggaattccaaatgcaaaatgcaagcttcgaagcaagaaac 235

RESULT 39
AF289417 291 bp DNA BCT 02-SEP-2000
LOCUS Helicobacter pylori isolate CR42
DEFINITION (caga) gene, partial cds.
ACCESSION AF289417.1 GI:9964168
VERSION AF289417.1 GI:9964168
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori

REFERENCE
AUTHORS Ouchiallin, A., Urdaci, M., Sierra, R., Munoz, N.,
TITLES Composition and gene expression of the cag pathogenicity island in
Helicobacter pylori strains isolated from gastric carcinoma and
gastritis patients in Costa Rica
JOURNAL Unpublished
PAGES 1 to 291
COUNTRY Costa Rica
SUBMITTED (26-JUL-2000) Laboratory of Bacteriology, University of
Bordeaux 2, 146 rue Leo Saignat, Bordeaux 33076, France
FEATURES
SOURCE
ORGANISM Helicobacter pylori
REFERENCE AF289417 291 bp DNA BCT 02-SEP-2000
LOCUS Helicobacter pylori isolate CR42
DEFINITION (caga) gene, partial cds.
ACCESSION AF289417.1 GI:9964168
VERSION AF289417.1 GI:9964168
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori

DB 138 atttttcaagcttggaattccaaatgcaaaatgcaagcttcgaagcaagaaac 197
QY 948 cgaatcttggaattccaaatgcaaaatgcaagcttcgaagcaagaaac 985
DB 198 cgaatcttggaattccaaatgcaaaatgcaagcttcgaagcaagaaac 235

RESULT 39
AF289417 291 bp DNA BCT 02-SEP-2000
LOCUS Helicobacter pylori isolate CR42
DEFINITION (caga) gene, partial cds.
ACCESSION AF289417.1 GI:9964168
VERSION AF289417.1 GI:9964168
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori

REFERENCE
AUTHORS Ouchiallin, A., Urdaci, M., Sierra, R., Munoz, N.,
TITLES Composition and gene expression of the cag pathogenicity island in
Helicobacter pylori strains isolated from gastric carcinoma and
gastritis patients in Costa Rica
JOURNAL Unpublished
PAGES 1 to 291
COUNTRY Costa Rica
SUBMITTED (26-JUL-2000) Laboratory of Bacteriology, University of
Bordeaux 2, 146 rue Leo Saignat, Bordeaux 33076, France
FEATURES
SOURCE
ORGANISM Helicobacter pylori
REFERENCE AF289417 291 bp DNA BCT 02-SEP-2000
LOCUS Helicobacter pylori isolate CR42
DEFINITION (caga) gene, partial cds.
ACCESSION AF289417.1 GI:9964168
VERSION AF289417.1 GI:9964168
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori

RESULT 39
AF289417 291 bp DNA BCT 02-SEP-2000
LOCUS Helicobacter pylori isolate CR42
DEFINITION (caga) gene, partial cds.
ACCESSION AF289417.1 GI:9964168
VERSION AF289417.1 GI:9964168
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori

REFERENCE
AUTHORS Ouchiallin, A., Urdaci, M., Sierra, R., Munoz, N.,
TITLES Composition and gene expression of the cag pathogenicity island in
Helicobacter pylori strains isolated from gastric carcinoma and
gastritis patients in Costa Rica
JOURNAL Unpublished
PAGES 1 to 291
COUNTRY Costa Rica
SUBMITTED (26-JUL-2000) Laboratory of Bacteriology, University of
Bordeaux 2, 146 rue Leo Saignat, Bordeaux 33076, France
FEATURES
SOURCE
ORGANISM Helicobacter pylori
REFERENCE AF289417 291 bp DNA BCT 02-SEP-2000
LOCUS Helicobacter pylori isolate CR42
DEFINITION (caga) gene, partial cds.
ACCESSION AF289417.1 GI:9964168
VERSION AF289417.1 GI:9964168
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori

REFERENCE 1 (bases 1 to 449)
 TITLE Helicobacter pylori: epsilon subunit: Helicobacter group;
 JOURNAL J. Clin. Microbiol. 37 (7), 2306-2311 (1999)
 MEDLINE 99294773
 AUTHOR van Doorn L.J.
 TITLE Direct Submission
 JOURNAL Submitted (13-SEP-1999) van Doorn L.J., Molecular Biology, Delta
 Diagnostics Laboratory, R. de Graafweg 7, Delft, 2625 AD,
 NETHERLANDS

FEATURES
 source 1. 449
 /organism="Helicobacter pylori"
 /locus_tag="HPY152970"
 /country="Netherlands"
 gene 1. 449
 /gene="cagA"
 CDS 1..449
 /codon_start=1
 /product="CagA protein"
 /protein_id="P52355.1"
 /db_xref="GI:5851972"
 /translation="MTNINQDQTEAHPNPPFNNLQVAFYAVNADYDPOK
 PLYDNDNDNDFRISQLEERSNKLINPTKQPSDIDKSDNKLKALIDV
 ESSTSPFQDQRIPTFSVSNQDPSRINTHSINRPHRIQPP"
 BASE COUNT 166 a 100 c 70 g 115 t
 ORIGIN

Query Match 2.6% Score 156; DB 2; Length 449;
 Local Similarity 100.0%; Prem. No. 8.2e-63;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 838 tctatctgagtgagatctcccaagagcttccaaatctggagcagctacag 887
 Db 254 tctcatctgagtgagatctcccaagagcttccaaatctggagcagctacag 353
 Oy 888 aatttcacagatgggtgtccctcaaacagctcgtctaaatcacaaccagctacag 947
 Db 334 aattttcacaatgtccgtccctcaaacagctcgtctaaatcacaaccagctacag 413
 Oy 948 cggaaatttagagaaatctcctcaaacctccat 983
 Db 414 cccaatttttagcaaaatgtctcaaacctccat 449

RESULT 44
 LOCUS AF198472 286 bp DNA BCT 19-MAY-2000
 DEFINITION CagA (cagA) gene, partial cds.
 ACCESSION AF198472.1 GI:7246670
 VERSION AF198472.1 GI:7246670
 KEYWORDS
 SOURCE Helicobacter pylori.
 ORGANISM Helicobacter pylori.
 REFERENCE 1 (bases 1 to 286)
 AUTHORS van der Ende A., Pan Z.J., Bart A., van der Hulst R.W., Feller M.,
 Xiao S.D., Tytgat G.N. and Dankert J.
 TITLE Helicobacter pylori strain Penicillin associated protein
 JOURNAL Infect. Immun. 66 (5), 1822-1826 (1998)
 MEDLINE 98314000
 AUTHOR van der Ende A.
 TITLE Direct Submission
 JOURNAL Submitted (26-OCT-1999) Molecular Microbiology, Washington

REFERENCE 1 (bases 1 to 286)
 AUTHORS van der Ende A., Pan Z.J., Bart A., van der Hulst R.W., Feller M.,
 Xiao S.D., Tytgat G.N. and Dankert J.
 TITLE Helicobacter pylori strain Penicillin associated protein
 JOURNAL Infect. Immun. 66 (5), 1822-1826 (1998)
 MEDLINE 98314000
 AUTHOR van der Ende A.
 TITLE Direct Submission
 JOURNAL Submitted (26-OCT-1999) Molecular Microbiology, Washington

RESULT 43
 HPY152970 244 bp DNA BCT 08-SEP-1999
 DEFINITION Helicobacter pylori partial cagA gene for cytotoxin associated
 protein A.
 ACCESSION AJ252970.1 GI:5851971
 VERSION AJ252970.1 GI:5851971
 AUTHOR van der Ende A., Pan Z.J., Bart A., van der Hulst R.W., Feller M.,
 Xiao S.D., Tytgat G.N. and Dankert J.
 TITLE Helicobacter pylori strain Penicillin associated protein A.
 JOURNAL Infect. Immun. 66 (5), 1822-1826 (1998)
 MEDLINE 98314000
 AUTHOR van der Ende A.
 TITLE Direct Submission
 JOURNAL Submitted (26-OCT-1999) Molecular Microbiology, Washington

FEATURES
 source 1. 244
 /organism="Helicobacter pylori"
 /locus_tag="HPY152970"
 /country="Netherlands"
 gene 1. 244
 /gene="cagA"
 CDS 1..244
 /codon_start=1
 /product="CagA protein"
 /protein_id="P52355.1"
 /db_xref="GI:5851972"
 /translation="MTNINQDQTEAHPNPPFNNLQVAFYAVNADYDPOK
 PLYDNDNDNDFRISQLEERSNKLINPTKQPSDIDKSDNKLKALIDV
 ESSTSPFQDQRIPTFSVSNQDPSRINTHSINRPHRIQPP"
 BASE COUNT 95 a 50 c 50 g 50 t
 ORIGIN

Query Match 2.6% Score 154; DB 2; Length 244;
 Local Similarity 100.0%; Prem. No. 7.6e-62;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 838 tctatctgagtgagatctcccaagagcttccaaatctggagcagctacag 887
 Db 254 tctcatctgagtgagatctcccaagagcttccaaatctggagcagctacag 353
 Oy 888 aatttcacagatgggtgtccctcaaacagctcgtctaaatcacaaccagctacag 947
 Db 334 aattttcacaatgtccgtccctcaaacagctcgtctaaatcacaaccagctacag 413
 Oy 948 cggaaatttagagaaatctcctcaaacctccat 983
 Db 414 cccaatttttagcaaaatgtctcaaacctccat 449

RESULT 45
 AF198472 286 bp DNA BCT 19-MAY-2000
 DEFINITION CagA (cagA) gene, partial cds.
 ACCESSION AF198472.1 GI:7246670
 VERSION AF198472.1 GI:7246670
 KEYWORDS
 SOURCE Helicobacter pylori.
 ORGANISM Helicobacter pylori.
 REFERENCE 1 (bases 1 to 286)
 AUTHORS van der Ende A., Pan Z.J., Bart A., van der Hulst R.W., Feller M.,
 Xiao S.D., Tytgat G.N. and Dankert J.
 TITLE Helicobacter pylori strain Penicillin associated protein
 JOURNAL Infect. Immun. 66 (5), 1822-1826 (1998)
 MEDLINE 98314000
 AUTHOR van der Ende A.
 TITLE Direct Submission
 JOURNAL Submitted (26-OCT-1999) Molecular Microbiology, Washington

REFERENCE 1 (bases 1 to 286)
 AUTHORS van der Ende A., Pan Z.J., Bart A., van der Hulst R.W., Feller M.,
 Xiao S.D., Tytgat G.N. and Dankert J.
 TITLE Helicobacter pylori strain Penicillin associated protein
 JOURNAL Infect. Immun. 66 (5), 1822-1826 (1998)
 MEDLINE 98314000
 AUTHOR van der Ende A.
 TITLE Direct Submission
 JOURNAL Submitted (26-OCT-1999) Molecular Microbiology, Washington

Tue Mar 27 09:32:16 2001

us-09-410-835-4.011g.rg

Page 127

Tue Mar 27 09:32:16 2001

us-09-410-835-4.011g.rge

Page 121

CD8
 1. >291
 /gene="cagA"
 /locus="cagA"
 /organism="Helicobacter pylori"
 /protein_id="AAC09860.1"
 /db_xref="GI:3964177"
 /translation="IKNPITKKNVSDPINSNDLINDNLIDVSTKSPKCNOR
 TQPTTSWKNQNDSPKINSINRINRHTIDPPIIDQKNAEFLKAKAGAC"
 111 a
 /gene="cagA"
 /note="Region: tyrosine phosphorylation motif A"

BASE COUNT 111 a 62 c 40 g 78 t

Query Match 2.1% Score 133 DB 2 Length 291
 Best Local Similarity 100.0% Pred No 4.3e-47
 Matches 133: Conservative 0 Mismatches 0 Indels 0 Gaps 0

LOCUS HPY269885 449 bp DNA BCT 23-SEP-1999
 DEFINITION Helicobacter pylori partial cagA gene for CagA protein, isolate
 HPY269885 from The Netherlands.
 ACCESSION AJ269885.1 GI:5921347
 KEYWORDS cagA gene; CagA protein.
 SOURCE Helicobacter pylori.
 ORGANISM Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 Helicobacter.
 REFERENCE 1 (bases 1 to 449)
 van Doorn L.J., Figueiredo C., Sanna R., Blaser M.J. and Quint M.G.
 Distribution of Helicobacter pylori cagA gene are associated with
 vacA subtypes
 J. Clin. Microbiol. 37 (7), 2306-2311 (1999)

VERSION AJ239729.1 GI:4467776
 KEYWORDS cagA gene; cytotoxin associated protein A.
 DEFINITION Helicobacter pylori.
 ORGANISM Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 Helicobacter.
 REFERENCE 1 (bases 1 to 243)
 Achtman A.S., Berg D.E., Ito Y., Novelli G., Pan Z.J.,
 Suerauf S., Thompson S.A., Van Der Ende A. and Van Doorn L.J.
 Recombination and clonal groupings within Helicobacter pylori from
 different geographical regions
 J. Clin. Microbiol. 37 (3), 459-470 (1999)
 2 (bases 1 to 243)
 van der Ende A.
 Direct Submission
 Submitted (13-SEP-1999) van der Ende A., Medical Microbiology,
 Academic Medical Center, Meibergdreef 15, Amsterdam, 1105 AZ,
 NETHERLANDS
 FEATURES
 source 1. 449
 /organism="Helicobacter pylori"
 /locus="cagA"
 /db_xref="taxon:210"
 /country="Australia"
 gene 1. >243
 /gene="cagA"
 /codon_start=1
 /product="cytotoxin associated protein A"
 /protein_id="CAB37821.1"
 /db_xref="GI:4467776"
 /translation="IKNPITKKNVSDPINSNDLINDNLIDVSTKSPKCNOR
 TQPTTSWKNQNDSPKINSINRINRHTIDPPIIDQKNAEFLKAKAGAC"
 92 a
 /gene="cagA"
 /note="Region: tyrosine phosphorylation motif A"

BASE COUNT 92 a 45 c 51 g 55 t

Query Match 2.0% Score 119 DB 2 Length 243
 Best Local Similarity 100.0% Pred No 3.4e-45
 Matches 119: Conservative 0 Mismatches 0 Indels 0 Gaps 0

LOCUS HPY269887 449 bp DNA BCT 23-SEP-1999
 DEFINITION Helicobacter pylori partial cagA gene for CagA protein, isolate
 HPY269887 from The Netherlands.
 ACCESSION AJ269887.1 GI:5921371
 KEYWORDS cagA gene; CagA protein.
 SOURCE Helicobacter pylori.
 ORGANISM Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 Helicobacter.
 REFERENCE 1 (bases 1 to 449)
 van Doorn L.J., Figueiredo C., Sanna R., Blaser M.J. and Quint M.G.
 Distribution of Helicobacter pylori cagA gene are associated with
 vacA subtypes
 J. Clin. Microbiol. 37 (7), 2306-2311 (1999)
 2 (bases 1 to 449)
 van der Ende A.
 Direct Submission
 Submitted (13-SEP-1999) van Doorn L.J., Molecular Biology, Delta
 Diagnostic Laboratory, R. de Graafweg 7, Delft, 2625 AD,
 NETHERLANDS
 FEATURES
 source 1. 449
 /organism="Helicobacter pylori"
 /locus="cagA"
 /db_xref="taxon:210"
 /country="Australia"
 gene 1. >449
 /gene="cagA"
 /codon_start=1
 /product="CagA protein"
 /protein_id="CAB37821.1"
 /db_xref="GI:5921371"
 /translation="IKNPITKKNVSDPINSNDLINDNLIDVSTKSPKCNOR
 TQPTTSWKNQNDSPKINSINRINRHTIDPPIIDQKNAEFLKAKAGAC"
 165 a
 /gene="cagA"
 /note="Region: tyrosine phosphorylation motif A"

HEADLINE 99294773
 REFERENCE 2 (bases 1 to 449)
 van Doorn L.J.
 TITLE Direct Submission
 JOURNAL Submitted (13-SEP-1999) van Doorn L.J., Molecular Biology, Delta
 Diagnostic Laboratory, R. de Graafweg 7, Delft, 2625 AD,
 NETHERLANDS
 FEATURES
 source 1. 449
 /organism="Helicobacter pylori"
 /locus="cagA"
 /db_xref="taxon:210"
 /country="Netherlands"
 gene 1. >449
 /gene="cagA"
 /codon_start=1
 /product="CagA protein"
 /protein_id="CAB37821.1"
 /db_xref="GI:5921348"
 /translation="IKNPITKKNVSDPINSNDLINDNLIDVSTKSPKCNOR
 TQPTTSWKNQNDSPKINSINRINRHTIDPPIIDQKNAEFLKAKAGAC"
 166 a
 /gene="cagA"
 /note="Region: tyrosine phosphorylation motif A"

BASE COUNT 166 a 94 c 70 g 119 t

Query Match 2.0% Score 121 DB 2 Length 449
 Best Local Similarity 99.4% Pred No 3.7e-46
 Matches 171: Conservative 0 Mismatches 1 Indels 0 Gaps 0

LOCUS HPY239729 243 bp DNA BCT 30-JUN-1999
 DEFINITION Helicobacter pylori partial cagA gene, strain NCTC11637.
 ACCESSION AJ239729

VERSION AJ239729.1 GI:4467776
 KEYWORDS cagA gene; cytotoxin associated protein A.
 DEFINITION Helicobacter pylori.
 ORGANISM Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 Helicobacter.
 REFERENCE 1 (bases 1 to 449)
 van Doorn L.J., Figueiredo C., Sanna R., Blaser M.J. and Quint M.G.
 Distribution of Helicobacter pylori cagA gene are associated with
 vacA subtypes
 J. Clin. Microbiol. 37 (7), 2306-2311 (1999)
 2 (bases 1 to 449)
 van der Ende A.
 Direct Submission
 Submitted (13-SEP-1999) van Doorn L.J., Molecular Biology, Delta
 Diagnostic Laboratory, R. de Graafweg 7, Delft, 2625 AD,
 NETHERLANDS
 FEATURES
 source 1. 449
 /organism="Helicobacter pylori"
 /locus="cagA"
 /db_xref="taxon:210"
 /country="Australia"
 gene 1. >449
 /gene="cagA"
 /codon_start=1
 /product="CagA protein"
 /protein_id="CAB37821.1"
 /db_xref="GI:5921372"
 /translation="IKNPITKKNVSDPINSNDLINDNLIDVSTKSPKCNOR
 TQPTTSWKNQNDSPKINSINRINRHTIDPPIIDQKNAEFLKAKAGAC"
 165 a
 /gene="cagA"
 /note="Region: tyrosine phosphorylation motif A"

	Query Match	1.9%	Coverage: 86	Length: 284	
	Best Local Similarity:	99.1%	Pred. No.: 27	d.f.: 1	
	Matches: 215	Conservative	0	Mismatches: 2	Indels: 0
Oy	1561	AACATGAGTGCCTCATCATTAAATGAAGTCATGGTAAGAAGAGCGGTGTTGATCATAGCA	1620		
Dd	68	AACATGTCGTCCATAAATTAATTCCTCATCTTGATAAAAACGCACTGCTCATCATACACC	127		
Oy	1621	GGTGGTCAATGAGGAGTATACCACTCAAGTTTCACTCTCCACAAGAGGCTCAACTCCA	1680		
Dd	128	GCTGCTCATTAACGCCATATACACCTCACTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC	187		
Oy	1681	ggctccacagcagaccatcaagcgccaagaagggtccacaacaaataagatttccttgaaattt	1740		
Dd	188	GGCTCCACAACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	247		
Oy	1741	cctgcacaaaactaacgctcaaatctgaacacctgaagacg	1777		
Dd	248	CTTCCACCAAAATTAATCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	284		
RESULT	86				
AF190660	3653 bp	DNA	BCT	04-OCT-2000	
DEFINITION	Helicobacter pylori strain 86-183 cag pathogenicity island polymorphic right end; type Ia motif; insertion sequence IS600, complete; and glutamate racemase (glut) gene, partial cds.				
ACCESSION	AF190660				
KEYWORDS	AF190660.1 GI:10567547				
SOURCE	Helicobacter pylori.				
ORGANISM	Helicobacter pylori.				
REFERENCE	Helicobacteriaceae; epsilon subdivision; Helicobacter group; Molecular Phylogenetic Analysis of Helicobacter Species 1. (bases 1 to 2863)				
AUTHORS	Kerstjens,D., Muhopadhyay,A.K., Velapatio,B., Su,W.W., Pan,Z.J., Garcia,C., Hernandez,V., Valdez,F., Marley,K.S., Glimm,R.H., Chowdhury,A., Datta,S., Shirai,M., Nakazawa,T., Alty,J.B., Segal,I., Wong,B.C., Lam,S.R., Olfert,P.O., Boretz,T., Bhargava,L., Torres,O., Schmidhaer,R., Thomas,J.E., Cohn,S., and Berg,D.E. Human population genomics of Helicobacter pylori from different J. Bacteriol. 187 (11), 3210-3218 (2005) 20270152				
JOURNAL	20050732				
MEDLINE	16093762				
REFERENCE	20050732, 1 to 2863)				
AUTHORS	and Berg,D.E., Muhopadhyay,A.K., Velapatio,B., Su,W.W., Pan,Z.J., Direct Substitution				

Tue Mar 27 09:32:16 2001

us-09-410-835-4.011g.rge

Page 183

RESULT	87	AF283939	291 bp	DN	RM	03-SEP-2000
AF283939		Helicobacter pylori isolate CRI cytotoxin associated protein A				
DEFINITION		(cgaA) gene, partial cds.				
ACCESSION		AF283939.1	GI:9664152			
VERSION						
KEYWORDS						
SOURCE						
ORGANISM		Helicobacter pylori.				
REFERENCE		Helicobacter pylori.				
TITLE		1 (bases 1 to 291)				
JOURNAL		Ouchaili, A., Megard, F., Urdaci, M., Sierra, R., Munoz, N.,				
REFERENCE		Correia, A. and Megard, F. Isolation of the cag pathogenicity island in				
AUTHORS		Helicobacter pylori strains isolated from gastric carcinoma and				
JOURNAL		gastritis patients in Costa Rica				
REFERENCE		Unpublished				
TITLE		2 (bases 1 to 291)				
JOURNAL		Ouchaili, A., Merla, A., Urdaci, M., Sierra, R., Munoz, N.,				
REFERENCE		Correia, A. and Megard, F.				
AUTHORS		Substrains 12/2000, Laboratory of Bacteriology, University of				
JOURNAL		Bordeaux 2, 145 rue Leo Saignat, Bordeaux 33076, France				
FEATURES		Location/Qualifiers				
source		1..291 gene=Helicobacter pylori.				
		/organism=Helicobacter pylori				
		/isolate=CRI				
		/db_xref=taxon:210*				
		/country=Costa Rica*				

```

FEATURES             SOURCE
126853 Helicobacter pylori*
  /organism="Helicobacter pylori"
  /db_xref="taxon:210"
  /strain="84-183"
  /map="between HP0547 and HP0549 in 26695 genome"
  /country="USA"
  /pathogenicity="pathogenic region at right end of the cag
  pathogenicity island"
  /type="molt": similar to
  Helicobacter pylori strain Gambia93/24 type II moltII
  presented in Genbank Accession Number AF390459"
  /size="15700"
  /note="similar to Helicobacter pylori insertion sequence
  15606"
  210.. 640
  /gene="putative DNA helicase"
  /description="Helicobacter pylori strain
  26695 putative helicase gene HP0548"
  739.. 2705
  /organism="Helicobacter pylori"
  /strain="84-183"
  /map="between HP0547 and HP0549 in 26695 genome"
  /insertion_seq="15606"
  /country="USA"
  /note="polymorphic region at right end of the cag
  pathogenicity island"
  /type="molt": similar to
  Helicobacter pylori insertion sequence
  15606 presented in Genbank Accession Number U95957"
  3765.. 3963
  /note="declines the terminus of the cag pathogenicity
  island"
  /type="direct"
  complement(2765.. >2963)
  /gene="glt"
  complement(2765.. >2863)
  /gene="glt"
  /note="similar to Helicobacter pylori strain 26695
  9000"
  /product="glutamate racemase"
  /strain="84-183"
  /protein_id="AAC1848.1"
  /translation="EEYRNHPALPPILLISGDIAIVETLQDVAALAKNNAPKPV
  EFHASDVITLQKQKPKMTI"
  566 c 531 g 849 t

```

Tue Mar 27 09:32:16 2001

us-09-410-835-4.011g.rge

Page 184

Query Match	Similarity	99.1%	Score 111	DB 2	Length 291
Accession	AF289416	1	GI:9964186		
Definition	Helicobacter pylori isolate CH38 cytotoxin associated protein A				
Accession	AF289416	1	GI:9964186		
Version					
Keywords	Helicobacter pylori				

gene /note="Isolated from a patient with chronic gastritis-associated dyspepsia"

CDS <1..>291
/gene="cagA"
/note="cagA"

FEATURES
source
Location/Qualifiers
1..291
/organism="Helicobacter pylori"
/db_xref="taxon:210"
/country="Costa Rica"
/note="Isolated from a patient with chronic gastritis associated dyspepsia"
/gene="cagA"
/db_xref="GI:9964137"
/transl_table=11
/product="cytochrome associated protein A"
/db_xref="GI:9964137"
/translation="IKNPTRKNVPSDFINSNDLINDKIDVSSSTFRKQDOR
VRIPTSVWQNDPSKIRTSIRNPHETIOPPIPDREKFLSKAKSFGAC"

misc_feature
/note="Region: tyrosine phosphorylation motif A"

BASE COUNT 106 a 61 c 46 g 78 t

ORIGIN

Query Match 1.7% Score 100; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 3.7e-36;
Matches 100: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 864 gaatttggagatcagcgttaccgatttccaaatggtggtccatccaaacagtc 923
|||||
Db 114 GAATTGGGATCAGCCTTACCCGATTTTCACAGTTGCGCTCCCATMAACATCC 173
|||||
Db 924 gcttaataatcaccacccgacgacgacgacgacgacgacgacgacgacgacgac 963
|||||
Db 174 GCTTAAATCACCACCCATCCATCCGAAATTTATGCA 213
|||||

RESULT 107

LOCUS AF289421 291 bp DNA BCT 02-SEP-2000

DEFINITION Helicobacter pylori isolate C850 cytotoxin associated protein A (cagA) gene, partial cds.

ACCESSION AF289421

VERSION AF289421.1 GI:9964136

KEYWORDS Helicobacter pylori.

SOURCE Helicobacter pylori.

ORGANISM Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group; Helicobacter.

REFERENCE 1 (bases 1 to 291)
Covacci, A. and Megraud, F.
Composition and gene expression of the cag pathogenicity island in Helicobacter pylori strains isolated from gastric carcinoma and

DEFINITION Helicobacter pylori isolate C854 cytotoxin associated protein A (cagA) gene, partial cds.

ACCESSION AF289425

VERSION AF289425.1 GI:9964204

KEYWORDS Helicobacter pylori.

SOURCE Helicobacter pylori.

ORGANISM Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group; Helicobacter.

REFERENCE 1 (bases 1 to 291)
Covacci, A. and Megraud, F.
Composition and gene expression of the cag pathogenicity island in Helicobacter pylori strains isolated from gastric carcinoma and

JOURNAL Unpublished

AUTHORS Covacci, A. and Megraud, F.

TITLE Helicobacter pylori strains isolated from gastric carcinoma and gastritis patients in Costa Rica

DEFINITION Helicobacter pylori isolate C854 cytotoxin associated protein A (cagA) gene, partial cds.

ACCESSION AF289427

VERSION AF289427.1 GI:9964208

KEYWORDS Helicobacter pylori.

SOURCE Helicobacter pylori.

ORGANISM Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group; Helicobacter.

REFERENCE 1 (bases 1 to 291)
Covacci, A. and Megraud, F.
Composition and gene expression of the cag pathogenicity island in Helicobacter pylori strains isolated from gastric carcinoma and

Query Match 1.7% Score 100; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 3.7e-36;

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 291)
Covacci, A. and Megraud, F.

TITLE Helicobacter pylori strains isolated from gastric carcinoma and gastritis patients in Costa Rica

JOURNAL Submitted (25-JUL-2000) Laboratory of Bacteriology, University of Bordeaux 2, 146 rue Leo Salgnat, Bordeaux 33076, France

FEATURES
source
Location/Qualifiers
1..291
/organism="Helicobacter pylori"
/isolate="C850"
/db_xref="taxon:210"
/country="Costa Rica"
/note="Isolated from a patient with chronic gastritis associated dyspepsia"
/gene="cagA"
/db_xref="GI:9964137"
/transl_table=11
/product="cytochrome associated protein A"
/db_xref="GI:9964137"
/translation="IKNPTRKNVPSDFINSNDLINDKIDVSSSTFRKQDOR
VRIPTSVWQNDPSKIRTSIRNPHETIOPPIPDREKFLSKAKSFGAC"

misc_feature
/note="Region: tyrosine phosphorylation motif A"

BASE COUNT 106 a 62 c 46 g 77 t

ORIGIN

Query Match 1.7% Score 100; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 3.7e-36;
Matches 100: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 864 gaatttggagatcagcgttaccgatttccaaatggtggtccatccaaacagtc 923
|||||
Db 114 GAATTGGGATCAGCCTTACCCGATTTTCACAGTTGCGCTCCCATMAACATCC 173
|||||
Db 924 gcttaataatcaccacccgacgacgacgacgacgacgacgacgacgacgacgac 963
|||||
Db 174 GCTTAAATCACCACCCATCCATCCGAAATTTATGCA 213
|||||

RESULT 108

LOCUS AF289425 291 bp DNA BCT 02-SEP-2000

DEFINITION Helicobacter pylori isolate C856 cytotoxin associated protein A (cagA) gene, partial cds.

ACCESSION AF289427

VERSION AF289427.1 GI:9964208

KEYWORDS Helicobacter pylori.

SOURCE Helicobacter pylori.

ORGANISM Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group; Helicobacter.

REFERENCE 1 (bases 1 to 291)
Covacci, A. and Megraud, F.
Composition and gene expression of the cag pathogenicity island in Helicobacter pylori strains isolated from gastric carcinoma and

DEFINITION Helicobacter pylori isolate C856 cytotoxin associated protein A (cagA) gene, partial cds.

ACCESSION AF289427

VERSION AF289427.1 GI:9964208

KEYWORDS Helicobacter pylori.

SOURCE Helicobacter pylori.

ORGANISM Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group; Helicobacter.

REFERENCE 1 (bases 1 to 291)
Covacci, A. and Megraud, F.
Composition and gene expression of the cag pathogenicity island in Helicobacter pylori strains isolated from gastric carcinoma and

JOURNAL Unpublished

AUTHORS Covacci, A. and Megraud, F.

TITLE Helicobacter pylori strains isolated from gastric carcinoma and gastritis patients in Costa Rica

DEFINITION Helicobacter pylori isolate C856 cytotoxin associated protein A (cagA) gene, partial cds.

ACCESSION AF289427

VERSION AF289427.1 GI:9964208

KEYWORDS Helicobacter pylori.

SOURCE Helicobacter pylori.

ORGANISM Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group; Helicobacter.

REFERENCE 1 (bases 1 to 291)
Covacci, A. and Megraud, F.
Composition and gene expression of the cag pathogenicity island in Helicobacter pylori strains isolated from gastric carcinoma and

Query Match 1.7% Score 100; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 3.7e-36;

/product="cytoxin associated protein A"
/protein_id="AAC09876.1"
/db_xref="GI:9664209"
/translation="IKNPRTKNQVFSDFIRNSNDLINDVSTSTSTFRFQDOR
/note="Isolated from a patient with chronic
gastritis associated dyspepsia"
115 113
misc_feature
/gene="cagA"
/note="Region: tyrosine phosphorylation motif A"

BASE COUNT 106 a 62 c 47 g 76 t

Query Match 1.7% Score 100; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 3,7e-36;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 864 gaatttcggagtcagcgttcacgaatttcgagtcacgaacacgacgc 923
DB 114 GAAATTTGCGCATACCGCTTACACAGTTGCTGCTCCATCAACCAATCC 173
QY 924 gctcaatcacacacgacgcacgacgaatttcagaa 963
DB 174 GCTTAAATCAACCCCATCAATCAATTTATGCA 213

RESULT 110
AF289428 291 bp DNA BCT 02-SEP-2000
LOCUS Helicobacter pylori isolate CHS7 cytoxin associated protein A
DEFINITION (cagA) gene, partial cds.
ACCESSION AF289428.1 GI:9664210
KEYWORDS
SOURCE
ORGANISM
Helicobacter pylori
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter pylori
Ochialini, A.; Marais, A.; Urdaci, M.; Sierra, R.; Munoz, N.;
Covacci, A. and Megraud, F.
Composition and gene expression of the cag pathogenicity island in
Helicobacter pylori strains isolated from gastric carcinoma and
gastritis patients in Costa Rica
Unpublished
2 (bases 1 to 291)
REFERENCE
Ochialini, A.; Marais, A.; Urdaci, M.; Sierra, R.; Munoz, N.;
Covacci, A. and Megraud, F.
TITLE
Direct Submision
Submitted (26-JUL-2000) Laboratory of Bacteriology, University of
Bordeaux 2, 146 rue Leo Saignes, Bordeaux 33076, France
LOCATION/Qualifiers

REFERENCE
Ochialini, A.; Marais, A.; Urdaci, M.; Sierra, R.; Munoz, N.;
Covacci, A. and Megraud, F.
TITLE
Composition and gene expression of the cag pathogenicity island in
Helicobacter pylori strains isolated from gastric carcinoma and
gastritis patients in Costa Rica
Unpublished
2 (bases 1 to 291)
REFERENCE
Ochialini, A.; Marais, A.; Urdaci, M.; Sierra, R.; Munoz, N.;
Covacci, A. and Megraud, F.
TITLE
Direct Submision
Submitted (26-JUL-2000) Laboratory of Bacteriology, University of
Bordeaux 2, 146 rue Leo Saignes, Bordeaux 33076, France
LOCATION/Qualifiers

REFERENCE
Ochialini, A.; Marais, A.; Urdaci, M.; Sierra, R.; Munoz, N.;
Covacci, A. and Megraud, F.
TITLE
Composition and gene expression of the cag pathogenicity island in
Helicobacter pylori strains isolated from gastric carcinoma and
gastritis patients in Costa Rica
Unpublished
2 (bases 1 to 291)
REFERENCE
Ochialini, A.; Marais, A.; Urdaci, M.; Sierra, R.; Munoz, N.;
Covacci, A. and Megraud, F.
TITLE
Direct Submision
Submitted (26-JUL-2000) Laboratory of Bacteriology, University of
Bordeaux 2, 146 rue Leo Saignes, Bordeaux 33076, France
LOCATION/Qualifiers

FEATURES
source
1 (bases 1 to 291)
/organism="Helicobacter pylori"
/isolate="CHS7"
/country="Costa Rica"
/note="Isolated from a patient with gastric
adenocarcinoma"
11. >291
CDS
/gene="cagA"
/note="cagA"
/codon_start=1
/product="cytoxin associated protein A"
/protein_id="AAC09876.1"
/db_xref="GI:9664210"
/translation="IKNPRTKNQVFSDFIRNSNDLINDVSTSTSTFRFQDOR
115 113
misc_feature
/gene="cagA"
/note="Region: tyrosine phosphorylation motif A"

BASE COUNT 109 a 60 c 44 g 78 t

Query Match 1.7% Score 98; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 3,4e-35;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 888 aatttcacacagtcgggtccacacgaatccgcctcaaacacacacgacgacg 947
DB 118 AATTTTCAGAGTGGCTGCTCCATCAACAGTTGCTGCTCCATCAACCAATCC 197
QY 948 cgaatttcac 985
DB 198 CGCAATTTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 215

source
1. 291
/organism="Helicobacter pylori"
/isolate="CHS7"
/db_xref="taxon:210"
/note="Isolated from a patient with chronic
gastritis associated dyspepsia"
115 113
misc_feature
/gene="cagA"
/note="cagA"
/codon_start=1
/product="cytoxin associated protein A"
/protein_id="AAC09877.1"
/db_xref="GI:9664211"
/translation="IKNPRTKNQVFSDFIRNSNDLINDVSTSTSTFRFQDOR
115 113
misc_feature
/gene="cagA"
/note="Region: tyrosine phosphorylation motif A"

BASE COUNT 106 a 62 c 46 g 77 t

Query Match 1.7% Score 100; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 3,7e-36;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 864 gaatttcggagtcagcgttcacgaatttcgagtcacgaacacgacgc 923
DB 114 GAAATTTGCGCATACCGCTTACACAGTTGCTGCTCCATCAACCAATCC 173
QY 924 gctcaatcacacacgacgcacgacgaatttcagaa 963
DB 174 GCTTAAATCAACCCCATCAATCAATTTATGCA 213

RESULT 111
AF289408 291 bp DNA BCT 02-SEP-2000
LOCUS Helicobacter pylori isolate CHS1 cytoxin associated protein A
DEFINITION (cagA) gene, partial cds.
ACCESSION AF289408.1 GI:9664170
KEYWORDS
SOURCE
ORGANISM
Helicobacter pylori
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter pylori
Ochialini, A.; Marais, A.; Urdaci, M.; Sierra, R.; Munoz, N.;
Covacci, A. and Megraud, F.
Composition and gene expression of the cag pathogenicity island in
Helicobacter pylori strains isolated from gastric carcinoma and
gastritis patients in Costa Rica
Unpublished
2 (bases 1 to 291)
REFERENCE
Ochialini, A.; Marais, A.; Urdaci, M.; Sierra, R.; Munoz, N.;
Covacci, A. and Megraud, F.
TITLE
Direct Submision
Submitted (26-JUL-2000) Laboratory of Bacteriology, University of
Bordeaux 2, 146 rue Leo Saignes, Bordeaux 33076, France
LOCATION/Qualifiers

RESULT 112
AF190995 897 bp DNA BCT 04-OCT-2000
LOCUS Helicobacter pylori strain Ohlo46 cag pathogenicity island
DEFINITION Polymorphic right end, type Ic motif left-end.
ACCESSION AF190995.1 GI:10657558
KEYWORDS
SOURCE
ORGANISM
Helicobacter pylori
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter pylori
Ochialini, A.; Marais, A.; Urdaci, M.; Sierra, R.; Munoz, N.;
Covacci, A. and Megraud, F.
TITLE
Composition and gene expression of the cag pathogenicity island in
Helicobacter pylori strains isolated from gastric carcinoma and
gastritis patients in Costa Rica
Unpublished
2 (bases 1 to 897)
REFERENCE
Ochialini, A.; Marais, A.; Urdaci, M.; Sierra, R.; Munoz, N.;
Covacci, A. and Megraud, F.
TITLE
Direct Submision
Submitted (01-OCT-1999) Molecular Microbiology, Washington
University Medical School, 4566 Scott Ave., St. Louis, MO 63110,
USA
LOCATION/Qualifiers

FEATURES
source
1. 897
/organism="Helicobacter pylori"
/strain="Ohlo46"
/db_xref="taxon:210"
/note="Isolated from a patient with chronic
gastritis associated dyspepsia"
115 113
misc_feature
/gene="cagA"
/note="cagA"
/codon_start=1
/product="cytoxin associated protein A"
/protein_id="AAC09877.1"
/db_xref="GI:9664211"
/translation="IKNPRTKNQVFSDFIRNSNDLINDVSTSTSTFRFQDOR
115 113
misc_feature
/gene="cagA"
/note="Region: tyrosine phosphorylation motif A"

BASE COUNT 310 a 170 c 152 g 265 t

Query Match 1.6% Score 97; DB 1; Length 897;
Best Local Similarity 100.0%; Pred. No. 9,3e-35;
QY 888 aatttcacacagtcgggtccacacgaatccgcctcaaacacacacgacgacg 947
DB 118 AATTTTCAGAGTGGCTGCTCCATCAACAGTTGCTGCTCCATCAACCAATCC 197
QY 948 cgaatttcac 985
DB 198 CGCAATTTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 215


```

source
1. 291
/organism="Helicobacter pylori"
/locus="CR39"
/db.xref="taxon:210"
/country="Costa Rica"
/note="Isolated from a patient with chronic gastritis associated dyspepsia"
<1..>291
/gene="cagA"
<1..>291
/gene="cagA"
/codon.start=1
/product="cytoxin associated protein A"
/translation="TTPKPKNQVSDPINSNDLINDVLSSTSPKPKDOR
YRITSWSHNDPPIKINSINRIPHIPTIDDEKKAFLKASQSFAC"
115..115
/note="Region: tyrosine phosphorylation motif A"
misc_feature
115..115
/region="Region: tyrosine phosphorylation motif A"
BASE COUNT 105 a 62 c 46 g 78 t
ORIGIN
Query Match 1.5% Score 89; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 6.4e-31;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 751 ATCAAAATCTCCGCAAAAGATGATTTTCAGATTCATCAATAGAGCATGAT 810
Db 1 ATCAAAATCTCCGCAAAAGATGATTTTCAGATTCATCAATAGAGCATGAT 60
QY 811 TATACCAAGAGATGATTTTCAGATTTTCAGATTTTCAGATTTTCAGAT 839
Db 61 TATACCAAGAGATGATTTTCAGATTTTCAGATTTTCAGATTTTCAGAT 89

```

```

RESULT 124
AF289426 291 bp DNA BCT 02-SEP-2000
LOCUS Helicobacter pylori isolate CR35 cytoxin associated protein A
AF289426.1 GI:9964206
ACCESSION AF289426.1 GI:9964206
VERSION AF289426.1 GI:9964206
KEYWORDS
SOURCE Helicobacter pylori.
ORGANISM Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
REFERENCE 1 (bases 1 to 291)
AUTHORS Occhialini,A., Marais,A., Urdaci,M., Sierra,R., Munoz,N.,
Covacci,A. and Megraud,F.
TITLE Helicobacter pylori strains isolated from gastric carcinoma and
gastritis patients in Costa Rica
JOURNAL 2 (bases 1 to 291)
AUTHORS Occhialini,A., Marais,A., Urdaci,M., Sierra,R., Munoz,N.,
Covacci,A. and Megraud,F.
TITLE Direct Submission (2000) Laboratory of Bacteriology, University of
Bordeaux 2, 146 rue Leo Saignat, Bordeaux 33076, France
FEATURES
source
1. 291
/organism="Helicobacter pylori"
/locus="CR35"
/db.xref="taxon:210"
/country="Costa Rica"
/note="Isolated from a patient with chronic gastritis associated dyspepsia"
<1..>291
/gene="cagA"
<1..>291
/gene="cagA"
/codon.start=1
/product="cytoxin associated protein A"
/translation="TTPKPKNQVSDPINSNDLINDVLSSTSPKPKDOR
YRITSWSHNDPPIKINSINRIPHIPTIDDEKKAFLKASQSFAC"
115..115
/note="Region: tyrosine phosphorylation motif A"
misc_feature
115..115
/region="Region: tyrosine phosphorylation motif A"
BASE COUNT 106 a 61 c 47 g 77 t

```

```

REFERENCE 1 (bases 1 to 291)
AUTHORS Occhialini,A., Marais,A., Urdaci,M., Sierra,R., Munoz,N.,
Covacci,A. and Megraud,F.
TITLE Helicobacter pylori strains isolated from gastric carcinoma and
gastritis patients in Costa Rica
JOURNAL 2 (bases 1 to 291)
AUTHORS Occhialini,A., Marais,A., Urdaci,M., Sierra,R., Munoz,N.,
Covacci,A. and Megraud,F.
TITLE Direct Submission (2000) Laboratory of Bacteriology, University of
Bordeaux 2, 146 rue Leo Saignat, Bordeaux 33076, France
FEATURES
source
1. 291
/organism="Helicobacter pylori"
/locus="CR35"
/db.xref="taxon:210"
/country="Costa Rica"
/note="Isolated from a patient with chronic gastritis associated dyspepsia"
<1..>291
/gene="cagA"
<1..>291
/gene="cagA"
/codon.start=1
/product="cytoxin associated protein A"
/translation="TTPKPKNQVSDPINSNDLINDVLSSTSPKPKDOR
YRITSWSHNDPPIKINSINRIPHIPTIDDEKKAFLKASQSFAC"
115..115
/note="Region: tyrosine phosphorylation motif A"
misc_feature
115..115
/region="Region: tyrosine phosphorylation motif A"
BASE COUNT 106 a 58 c 46 g 79 t
ORIGIN
Query Match 1.5% Score 89; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.9e-30;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 751 ATCAAAATCTCCGCAAAAGATGATTTTCAGATTCATCAATAGAGCATGAT 810
Db 1 ATCAAAATCTCCGCAAAAGATGATTTTCAGATTCATCAATAGAGCATGAT 60
QY 811 TATACCAAGAGATGATTTTCAGATTTTCAGATTTTCAGATTTTCAGAT 839
Db 61 TATACCAAGAGATGATTTTCAGATTTTCAGATTTTCAGATTTTCAGAT 89

```

```

RESULT 125
AF289441 678 bp DNA BCT 02-SEP-2000
LOCUS Helicobacter pylori isolate CR13 cytoxin associated protein A
AF289441.1 GI:9964216
ACCESSION AF289441.1 GI:9964216
VERSION AF289441.1 GI:9964216
KEYWORDS
SOURCE Helicobacter pylori.
ORGANISM Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
REFERENCE 1 (bases 1 to 678)
AUTHORS Occhialini,A., Marais,A., Urdaci,M., Sierra,R., Munoz,N.,
Covacci,A. and Megraud,F.
TITLE Helicobacter pylori strains isolated from gastric carcinoma and
gastritis patients in Costa Rica
JOURNAL 2 (bases 1 to 678)
AUTHORS Occhialini,A., Marais,A., Urdaci,M., Sierra,R., Munoz,N.,
Covacci,A. and Megraud,F.
TITLE Direct Submission (2000) Laboratory of Bacteriology, University of
Bordeaux 2, 146 rue Leo Saignat, Bordeaux 33076, France
FEATURES
source
1. 678
/organism="Helicobacter pylori"
/locus="CR13"
/db.xref="taxon:210"
/country="Costa Rica"
/note="Isolated from a patient with gastric adenocarcinoma"
<1..>678
/gene="cagA"
<1..>678
/gene="cagA"

```



```

LOCUS      AF289439       570 bp      DNA      BCT
DEFINITION Helicobacter pylori isolate C93 cytotoxin associated protein A
ACCESSION  AF289439.1
VERSION    AF289439.1 GI:9964232
KEYWORDS
SOURCE      Helicobacter pylori.
            Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
            Helicobacter.
REFERENCE   1 (bases 1 to 570)
            Ouchaili,A., Marita,A., Urdaci,M., Sierra,R., Munoz,N.,
            Helicobacter group: characterization of the cytotoxin associated
            protein A gene expression of the cag pathogenicity island in
            Helicobacter pylori strains isolated from gastric carcinoma and
            gastritis patients in Costa Rica
            2 (bases 1 to 570)
            Ouchaili,A., and Merisand,F.,
            Covacci,A., and Megraud,F.,
            Direct Submission (2001) Laboratory of Bacteriology, University of
            Bordeaux 2, 146 rue Leo Slagter, Bordeaux 33076, France
FEATURES
            source
            location/Qualifiers
            1..570      /gene="helicobacter_pylori"
                    /isolate="C93"
                    /db_xref="taxon:210"
                    /country="Costa Rica"
                    /note="Isolated from a patient with gastric
                    <1..>570
                    /gene="cagA"
                    <1..>570
                    /note="cagA"
                    /codon_start=1
                    /format="table"
                    /product="cytotoxin associated protein A"
                    /translation="PEERITIAAKVAKVADIKLNQIASGIVGQADAPPIKRIIDRIVSGVSPER
                    TIDTDSLTSTNPKVYSKATVATLNN"
            101..c      125 g      138 t
Query Match      1.44; Score 85; DB 2; Length 570;
Best Local Similarity 99.3%; Pred. No. 4.9e-29;

```

[illegible]

Tue Mar 27 09:32:16 2001

us-09-410-835-4.011g.rge

Page 267

Tue Mar 27 09:32:16 2001

us-09-410-835-4.011g.rge

Page 26B

Tue Mar 27 09:32:16 2001

us-09-410-835-4.011g.rge

Page 271

Tue Mar 27 09:32:16 2001

us-09-410-835-4.011g.rge

Page 272

FEATURES	source
JOURNAL	Sierstadius S., Thompson S.A., Van Der Ende A. and Van Doorn L.J.
MEDLINE	99255683
REFERENCE	2 (base 1 to 243)
FEATURES	Direct Submission
TITLE	Submitted (23-FEB-1999) van der Ende A., Medical Microbiology,
JOURNAL	Academic Medical Center, Meibergdreef 15, Amsterdam, 1105 AZ,
	NETHERLANDS
	Location/Qualifiers
	243
	/organism="Helicobacter pylori"
	/strain="N6"
	/accession="F030N.210"
	/country="France"
	1. 243
	<1..>"caga"
	/gene="caga"
	/codon_start=1
	/transl_table=1
	/product="Cytotoxin associated protein A"
	/protein_id="CA31812.1"
	/db_xref="GenBank:U093165"
	/translation="VGVDQGGNNVAVITVHKRGGCGVLAQGGKINPFFLYLKE
	DOLNQAAGSCEVLEININRDIPEPLNANLNADLSE"
	93 a 40 c 51 g 58 t
BASE COUNT	
ORIGIN	
Query Match	1..11. Score 64. Db 2. Length 243:
Best Local Similarity	100.0% P: 0.0000000000000000
Matches 64:	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	1776 caga 1779
DB	180 AACCAATATTCATTCGATTCTTCGCAATATGCTAACTAGCAACTG 239
DB	240 CAGG 243
DB	243 bp DNA
DB	Helicobacter pylori partial caga gene, strain 581.
DB	Accession AJ339731

```

/Note=This sequence differs from type I strains such as
399 and Gambia which contain a putative hellicase gene at
this location.
/Note=defines the terminus of the cag pathogenicity
island.
/rps_type=direct
/rps_score=91.460...9633)
/gene=gli1460...
/Note=Flanks cag pathogenicity island*
complement(460...9633)
/gene=gli1460...
/Note=Similar to Helicobacter pylori strain 26695
glutamate receptor mp05499
/codon_start=3
/tranai_label=11
/tranai_label=11
/protein_id=AA014645.1
/db_xref=GI:10567552.1
/tranai_label=CYPHEMFLTPPLHSGDAIVELYLOKVALKNHMFYKWEV
HAGSDVLEKQAKLQKML*
BASE COUNT      189 a      107 c      149 g      208 t

Query Match
Description: Similarity 100.00% (P=0.00)
Matches: 65; Conservative: 0; Mismatches: 10; Indels: 0; Gaps: 0.

Cy 4308 ctttaataatccgcagacacacacacacgaaaggtcttctctcctaagcgcgataagat 4367
Db 46 ctttaataatccgcagacacacacacacgaaaggtcttctctcctaagcgcgataagat 4367
Cy 4368 tttcc 4372
Db 106 tttcc 110

RESULT 177
LOCUS      HPY319720
DEFINITION Helicobacter pylori partial cagA gene, strain N6.
ACCESSION AJ2319720
VERSION    AJ2319720.1
KEYWORDS   Helicobacter pylori, cagA gene, associated protein A.
SOURCE     Helicobacter pylori
ORGANISM   Helicobacter pylori
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
1 (bases 1 to 243)
Author's   Achtman, M., Azuma, T., Berg, D.E., Ito, Y., Morelli, G., Pan, E.J.,

```

Tue Mar 27 09:32:16 2001

us-09-410-835-4.01lg.rge

Page 315

Tue Mar 27 09:32:16 2001

us-09-410-835-4.011g.rge

Page 320

Tue Mar 27 09:32:16 2001

us-09-410-835-4.011g.rge

Page 320

Tue Mar 27 09:32:16 2001

us-09-410-835-4.011g.rge

Page 331

Tue Mar 27 09:32:16 2001

us-09-410-835-4.011g.rge

Page 332

Query Match 1.00; Score 57; DB 2; Length 513;
 Best Local Similarity 100.00; Pred. No. 1e-15;
 Matches 57; Conservative 0; Mismatches 0; Gaps 0;
 3358 ttcacccttgaaagcagcatgaatgatccagctaaagtcagcccttcacagg 3414

Tue Mar 27 09:32:16 2001

us-09-410-835-4.011g.rge

Page 332

DB 283 TCCCTTGAAGAAACGCTATTAATGTCATCTTCAGTACAGGCTTACAG 319

RESULT 189
AF289452
LOCUS AF289452
DEFINITION Helicobacter pylori isolate CR48 cytotoxin associated protein A
ACCESSION AF289452
VERSION AF289452.1 GI:9696428
KEYWORDS
SOURCE ORGANISM
Helicobacter pylori
Helicobacter pylori
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Dochsalini A, Mearls A., Urdaci M., Sierra R., Munoz N.,
Covecci A. and Megraud F.
Composition and gene expression of the cag pathogenicity island in
gastric Helicobacter pylori strains isolated from gastric carcinomas and
gastritis patients in Costa Rica
Unpublished
2. (bases 1 to 567)
Covecci A. and Mearls A., Urdaci M., Sierra R., Munoz N.,
Covecci A. and Megraud F.
Direct Submission
Submitted (26-SEP-2000) Laboratory of Bacteriology, University of
Bordeaux II, UMR 5070, Laboratoire de Microbiologie, Bordeaux 33076, France
Location/Availability
1. -567

```

/isolate="CH46"
/submitter="Costa Rica"
/db_xref="taxon:210"
/country="Costa Rica"
/notes="isolated from a patient with chronic
gastritis-associated dyspepsia"
<I. >3587
/gene="cagA"
<I. >3587
CDS

```

```

MEDLINE      108070153
PUBMED      108070153
KEYWORDS    Helicobacter pylori, Kersulaye, D., Chowdhury, A., Dutta, S., Mallick, B.,
AUTHORS     Mukhopadhyay, A.K., Kersulaye, D., Chowdhury, A., Dutta, S., Mallick, B.,
            and Berg, D.E.
TITLE       Direct Submission
JOURNAL     Submitted (08/06/2009) Molecular Microbiology, Washington
            University, 10860 University Ave., St. Louis, MO 63110, USA
FEATURES    location/Qualifiers
            1..286
            /organism=Helicobacter pylori
            /db_xref=indol1210*
            <1..-286
            /gene=csaA*
            <1..-286
            /note=Helicobacter pylori 26695 HPO547*
            /codon_table=1
            /rname=csaA
            /protein_id=AA042877.1
            /protein_id=AA042877.1
            /db_xref=GI:7229442*
            /translation=MGCGDGRNDNNVATIGDGGCHNATITIVHKKNSGIVLAGQ
            EKGINRSLPTKEDYICGSQLALSGEIRKIRIDPEFLAQNMAKLDSL*
            103 a
            21 c
            57 g
            64 t
            0.9%
            Score 56, DP 3, length 286;
            Best Local Similarity 100.0%, Pval No. 3, e-15;
            Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0
            0y 1642 AACCTAGTTTATCTCTACGAAGAAGAGCAACTACAGCTACCAAGAGCAT 1657
            Db 148 AACCTAGTTTATCTCTACGAAGAAGAGCAACTACAGCTACCAAGCAT 201

RESULT 192
AF2032219
LOCUS      287 bp          DNA
DEFINITION Helicobacter pylori strain Ind183 csaA (csaA) gene, partial cda.
VERSION    AF2032219
VERSION    AF2032219
KEYWORDS   Helicobacter pylori.
SOURCE     Helicobacter pylori.
ORGANISM   Helicobacter pylori.
            Helicobacter pylori.
            Helicobacter pylori.
            Helicobacter group:
            Helicobacter
            1 (base 1 to 287)
            Mukhopadhyay, A.K., Kersulaye, D., Jeong, J.Y., Dutta, S., Ito, Y.,

```

```

Query Match      0.94; Score 56; DB 2; length 464;
Best Local Similarity 100.0%; Pred. No. 3,1e-15;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```


25.389(6649):4121)
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 SOURCE
 1. 10482
 /organism="Helicobacter pylori 26695"
 /strain="26695"
 /db_xref="GI:2136821"
 /gene="HP0556"
 /complement(67, 504)
 /note="hypothetical protein; identified by Genbank;
 putative"
 /codon_start=1
 /product="H. pylori predicted coding region HP0556"
 /protein_id="AA007625.1"
 /db_xref="GI:2136821"
 /translation="VYTHKIKRPSNWSILNRGRFASVFFSLVITVNSS
 AVALAPHLQPLISFSGFVADAPKSKIFPTFRISVCSLLALPAH
 complement(97), 1911)
 /gene="HP0557"
 /complement(97, 1911)
 /note="HP0557 to GB:U6394 SP:P1087 P1D:110996
 P1D:117322 P1D:112205 percent identity: 50.33. Identified
 by sequence similarity: putative"
 /codon_start=1
 /translation="MAVILDFEMIKNEIQLINLQDREKILKRLDFEWSI
 /db_xref="GI:213675"
 /translation="MAVILDFEMIKNEIQLINLQDREKILKRLDFEWSI
 /db_xref="GI:213675"

25.389(6649):4121)
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 SOURCE
 1. 10482
 /organism="Helicobacter pylori 26695"
 /strain="26695"
 /db_xref="GI:2136821"
 /gene="HP0556"
 /complement(67, 504)
 /note="hypothetical protein; identified by Genbank;
 putative"
 /codon_start=1
 /product="H. pylori predicted coding region HP0556"
 /protein_id="AA007625.1"
 /db_xref="GI:2136821"
 /translation="VYTHKIKRPSNWSILNRGRFASVFFSLVITVNSS
 AVALAPHLQPLISFSGFVADAPKSKIFPTFRISVCSLLALPAH
 complement(97), 1911)
 /gene="HP0557"
 /complement(97, 1911)
 /note="HP0557 to GB:U6394 SP:P1087 P1D:110996
 P1D:117322 P1D:112205 percent identity: 50.33. Identified
 by sequence similarity: putative"
 /codon_start=1
 /translation="MAVILDFEMIKNEIQLINLQDREKILKRLDFEWSI
 /db_xref="GI:213675"
 /translation="MAVILDFEMIKNEIQLINLQDREKILKRLDFEWSI
 /db_xref="GI:213675"

25.389(6649):4121)
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 SOURCE
 1. 10482
 /organism="Helicobacter pylori 26695"
 /strain="26695"
 /db_xref="GI:2136821"
 /gene="HP0556"
 /complement(67, 504)
 /note="hypothetical protein; identified by Genbank;
 putative"
 /codon_start=1
 /product="H. pylori predicted coding region HP0556"
 /protein_id="AA007625.1"
 /db_xref="GI:2136821"
 /translation="VYTHKIKRPSNWSILNRGRFASVFFSLVITVNSS
 AVALAPHLQPLISFSGFVADAPKSKIFPTFRISVCSLLALPAH
 complement(97), 1911)
 /gene="HP0557"
 /complement(97, 1911)
 /note="HP0557 to GB:U6394 SP:P1087 P1D:110996
 P1D:117322 P1D:112205 percent identity: 50.33. Identified
 by sequence similarity: putative"
 /codon_start=1
 /translation="MAVILDFEMIKNEIQLINLQDREKILKRLDFEWSI
 /db_xref="GI:213675"
 /translation="MAVILDFEMIKNEIQLINLQDREKILKRLDFEWSI
 /db_xref="GI:213675"

25.389(6649):4121)
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 SOURCE
 1. 10482
 /organism="Helicobacter pylori 26695"
 /strain="26695"
 /db_xref="GI:2136821"
 /gene="HP0556"
 /complement(67, 504)
 /note="hypothetical protein; identified by Genbank;
 putative"
 /codon_start=1
 /product="H. pylori predicted coding region HP0556"
 /protein_id="AA007625.1"
 /db_xref="GI:2136821"
 /translation="VYTHKIKRPSNWSILNRGRFASVFFSLVITVNSS
 AVALAPHLQPLISFSGFVADAPKSKIFPTFRISVCSLLALPAH
 complement(97), 1911)
 /gene="HP0557"
 /complement(97, 1911)
 /note="HP0557 to GB:U6394 SP:P1087 P1D:110996
 P1D:117322 P1D:112205 percent identity: 50.33. Identified
 by sequence similarity: putative"
 /codon_start=1
 /translation="MAVILDFEMIKNEIQLINLQDREKILKRLDFEWSI
 /db_xref="GI:213675"
 /translation="MAVILDFEMIKNEIQLINLQDREKILKRLDFEWSI
 /db_xref="GI:213675"

25.389(6649):4121)
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 SOURCE
 1. 10482
 /organism="Helicobacter pylori 26695"
 /strain="26695"
 /db_xref="GI:2136821"
 /gene="HP0556"
 /complement(67, 504)
 /note="hypothetical protein; identified by Genbank;
 putative"
 /codon_start=1
 /product="H. pylori predicted coding region HP0556"
 /protein_id="AA007625.1"
 /db_xref="GI:2136821"
 /translation="VYTHKIKRPSNWSILNRGRFASVFFSLVITVNSS
 AVALAPHLQPLISFSGFVADAPKSKIFPTFRISVCSLLALPAH
 complement(97), 1911)
 /gene="HP0557"
 /complement(97, 1911)
 /note="HP0557 to GB:U6394 SP:P1087 P1D:110996
 P1D:117322 P1D:112205 percent identity: 50.33. Identified
 by sequence similarity: putative"
 /codon_start=1
 /translation="MAVILDFEMIKNEIQLINLQDREKILKRLDFEWSI
 /db_xref="GI:213675"
 /translation="MAVILDFEMIKNEIQLINLQDREKILKRLDFEWSI
 /db_xref="GI:213675"

25.389(6649):4121)
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 SOURCE
 1. 10482
 /organism="Helicobacter pylori 26695"
 /strain="26695"
 /db_xref="GI:2136821"
 /gene="HP0556"
 /complement(67, 504)
 /note="hypothetical protein; identified by Genbank;
 putative"
 /codon_start=1
 /product="H. pylori predicted coding region HP0556"
 /protein_id="AA007625.1"
 /db_xref="GI:2136821"
 /translation="VYTHKIKRPSNWSILNRGRFASVFFSLVITVNSS
 AVALAPHLQPLISFSGFVADAPKSKIFPTFRISVCSLLALPAH
 complement(97), 1911)
 /gene="HP0557"
 /complement(97, 1911)
 /note="HP0557 to GB:U6394 SP:P1087 P1D:110996
 P1D:117322 P1D:112205 percent identity: 50.33. Identified
 by sequence similarity: putative"
 /codon_start=1
 /translation="MAVILDFEMIKNEIQLINLQDREKILKRLDFEWSI
 /db_xref="GI:213675"
 /translation="MAVILDFEMIKNEIQLINLQDREKILKRLDFEWSI
 /db_xref="GI:213675"

25.389(6649):4121)
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 SOURCE
 1. 10482
 /organism="Helicobacter pylori 26695"
 /strain="26695"
 /db_xref="GI:2136821"
 /gene="HP0556"
 /complement(67, 504)
 /note="hypothetical protein; identified by Genbank;
 putative"
 /codon_start=1
 /product="H. pylori predicted coding region HP0556"
 /protein_id="AA007625.1"
 /db_xref="GI:2136821"
 /translation="VYTHKIKRPSNWSILNRGRFASVFFSLVITVNSS
 AVALAPHLQPLISFSGFVADAPKSKIFPTFRISVCSLLALPAH
 complement(97), 1911)
 /gene="HP0557"
 /complement(97, 1911)
 /note="HP0557 to GB:U6394 SP:P1087 P1D:110996
 P1D:117322 P1D:112205 percent identity: 50.33. Identified
 by sequence similarity: putative"
 /codon_start=1
 /translation="MAVILDFEMIKNEIQLINLQDREKILKRLDFEWSI
 /db_xref="GI:213675"
 /translation="MAVILDFEMIKNEIQLINLQDREKILKRLDFEWSI
 /db_xref="GI:213675"

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

On nucleic - nucleic search, using av model

Run on: March 26, 2001, 14:45:04 ; Search time 371.66 seconds
(without alignments)

Title: US-09-410-835-4
Sequence: 1 cccatttgcacaccca.....tttcgacacacacgctt 5925

Scoring table:

Gap: 50.0 ; Gap: 60.0
Gap: 480022 seqs, 18783333 residues

Word size: 15

Total number of hits satisfying chosen parameters: 8150

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database: N:GenSeq_16.1
1: /cgnl_8/gcgdate/geneseq/geneseq/NA1980.DAT
2: /cgnl_8/gcgdate/geneseq/geneseq/NA1981.DAT
3: /cgnl_8/gcgdate/geneseq/geneseq/NA1982.DAT
4: /cgnl_8/gcgdate/geneseq/geneseq/NA1983.DAT
5: /cgnl_8/gcgdate/geneseq/geneseq/NA1984.DAT
6: /cgnl_8/gcgdate/geneseq/geneseq/NA1985.DAT
7: /cgnl_8/gcgdate/geneseq/geneseq/NA1986.DAT
8: /cgnl_8/gcgdate/geneseq/geneseq/NA1987.DAT
9: /cgnl_8/gcgdate/geneseq/geneseq/NA1988.DAT
10: /cgnl_8/gcgdate/geneseq/geneseq/NA1989.DAT
11: /cgnl_8/gcgdate/geneseq/geneseq/NA1990.DAT
12: /cgnl_8/gcgdate/geneseq/geneseq/NA1991.DAT
13: /cgnl_8/gcgdate/geneseq/geneseq/NA1992.DAT
14: /cgnl_8/gcgdate/geneseq/geneseq/NA1993.DAT
15: /cgnl_8/gcgdate/geneseq/geneseq/NA1994.DAT
16: /cgnl_8/gcgdate/geneseq/geneseq/NA1995.DAT
17: /cgnl_8/gcgdate/geneseq/geneseq/NA1996.DAT
18: /cgnl_8/gcgdate/geneseq/geneseq/NA1997.DAT
19: /cgnl_8/gcgdate/geneseq/geneseq/NA1998.DAT
20: /cgnl_8/gcgdate/geneseq/geneseq/NA1999.DAT
21: /cgnl_8/gcgdate/geneseq/geneseq/NA1000.DAT

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.mrg

Page 3

42 31 0.5 990 19 X14282 R. p101 GPO 174
43 27 0.5 36 21 Z50141 CAG 1 PCR primer f
44 26 0.4 18 21 V51312 H. p101 GPO 162
45 25 0.4 18 21 Z50142 H. p101 GPO 162
46 25 0.4 24 18 V51313 H. p101 GPO 162
47 24 0.4 24 18 V51313 H. p101 GPO 162
48 23 0.4 30 18 V45504 H. p101 GPO 162
49 22 0.4 24 18 V51312 H. p101 GPO 162
50 22 0.4 26 20 V90656 H. p101 GPO 162
51 22 0.4 26 20 V90656 H. p101 GPO 162
52 21 0.4 21 19 V73527 H. p101 GPO 162
53 21 0.4 1603 19 V73527 H. p101 GPO 162
54 21 0.4 2138 21 A14071 H. p101 GPO 162
55 21 0.4 20 18 V73527 H. p101 GPO 162
56 20 0.3 20 19 V73527 H. p101 GPO 162
57 20 0.3 20 19 V73527 H. p101 GPO 162
58 20 0.3 20 19 V73527 H. p101 GPO 162
59 20 0.3 20 19 V73527 H. p101 GPO 162
60 20 0.3 20 19 V73527 H. p101 GPO 162
61 20 0.3 284 15 Q18651 H. p101 GPO 162
62 20 0.3 284 15 Q18651 H. p101 GPO 162
63 20 0.3 619 21 A26931 H. p101 GPO 162
64 20 0.3 619 21 A26931 H. p101 GPO 162
65 20 0.3 1118 21 A09041 H. p101 GPO 162
66 20 0.3 1118 21 A09041 H. p101 GPO 162
67 20 0.3 1440 18 V75036 H. p101 GPO 162
68 20 0.3 1440 18 V75036 H. p101 GPO 162
69 20 0.3 1537 20 X90157 H. p101 GPO 162
70 20 0.3 1537 20 X90157 H. p101 GPO 162
71 20 0.3 1537 20 X90157 H. p101 GPO 162
72 20 0.3 1537 20 X90157 H. p101 GPO 162
73 20 0.3 1537 20 X90157 H. p101 GPO 162
74 20 0.3 1537 20 X90157 H. p101 GPO 162
75 20 0.3 1537 20 X90157 H. p101 GPO 162
76 20 0.3 1537 20 X90157 H. p101 GPO 162
77 20 0.3 1537 20 X90157 H. p101 GPO 162
78 20 0.3 1537 20 X90157 H. p101 GPO 162
79 20 0.3 1537 20 X90157 H. p101 GPO 162
80 20 0.3 1537 20 X90157 H. p101 GPO 162
81 20 0.3 1537 20 X90157 H. p101 GPO 162
82 20 0.3 1537 20 X90157 H. p101 GPO 162
83 20 0.3 1537 20 X90157 H. p101 GPO 162
84 20 0.3 1537 20 X90157 H. p101 GPO 162
85 20 0.3 1537 20 X90157 H. p101 GPO 162
86 20 0.3 1537 20 X90157 H. p101 GPO 162
87 20 0.3 1537 20 X90157 H. p101 GPO 162
88 20 0.3 1537 20 X90157 H. p101 GPO 162
89 20 0.3 1537 20 X90157 H. p101 GPO 162
90 20 0.3 1537 20 X90157 H. p101 GPO 162
91 20 0.3 1537 20 X90157 H. p101 GPO 162
92 20 0.3 1537 20 X90157 H. p101 GPO 162

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.mrg

Page 2

Prod. No. is the number of results predicted by change to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
1	5925	100.0	5925	14	048713	NA gene	Helicobacter pylori
2	5925	100.0	19932	17	T646159	Helicobacter pylori	Helicobacter pylori
3	3444	58.1	4149	19	V73461	H. p101 GPO 162	H. p101 GPO 162
4	277	4.7	449	19	V73601	H. p101 GPO 162	H. p101 GPO 162
5	277	4.7	449	19	V73601	H. p101 GPO 162	H. p101 GPO 162
6	277	4.7	449	19	V73601	H. p101 GPO 162	H. p101 GPO 162
7	235	4.0	3648	15	064580	Helicobacter pylori	Helicobacter pylori
8	235	4.0	3648	15	064580	Helicobacter pylori	Helicobacter pylori
9	235	4.0	3648	15	064580	Helicobacter pylori	Helicobacter pylori
10	235	4.0	3648	15	064580	Helicobacter pylori	Helicobacter pylori
11	235	4.0	3648	15	064580	Helicobacter pylori	Helicobacter pylori
12	235	4.0	3648	15	064580	Helicobacter pylori	Helicobacter pylori
13	194	3.3	449	19	V73606	H. p101 GPO 162	H. p101 GPO 162
14	178	3.0	449	19	V73606	H. p101 GPO 162	H. p101 GPO 162
15	178	3.0	449	19	V73606	H. p101 GPO 162	H. p101 GPO 162
16	178	3.0	449	19	V73606	H. p101 GPO 162	H. p101 GPO 162
17	166	2.8	3549	18	T67410	H. p101 GPO 162	H. p101 GPO 162
18	166	2.8	3549	18	T67410	H. p101 GPO 162	H. p101 GPO 162
19	166	2.8	3549	18	T67410	H. p101 GPO 162	H. p101 GPO 162
20	136	2.3	449	19	V73605	H. p101 GPO 162	H. p101 GPO 162
21	131	2.2	449	19	V73612	H. p101 GPO 162	H. p101 GPO 162
22	131	2.2	449	19	V73612	H. p101 GPO 162	H. p101 GPO 162
23	131	2.2	449	19	V73612	H. p101 GPO 162	H. p101 GPO 162
24	131	2.2	449	19	V73612	H. p101 GPO 162	H. p101 GPO 162
25	110	1.9	285	20	V90548	H. p101 GPO 162	H. p101 GPO 162
26	110	1.9	285	20	V90548	H. p101 GPO 162	H. p101 GPO 162
27	110	1.9	285	20	V90548	H. p101 GPO 162	H. p101 GPO 162
28	110	1.9	285	20	V90548	H. p101 GPO 162	H. p101 GPO 162
29	110	1.9	285	20	V90548	H. p101 GPO 162	H. p101 GPO 162
30	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
31	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
32	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
33	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
34	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
35	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
36	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
37	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
38	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
39	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
40	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
41	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
42	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
43	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
44	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
45	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
46	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
47	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
48	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
49	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
50	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
51	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
52	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
53	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
54	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
55	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
56	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
57	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
58	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
59	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
60	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
61	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
62	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
63	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
64	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
65	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
66	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
67	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
68	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
69	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
70	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
71	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
72	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
73	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
74	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
75	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
76	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
77	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
78	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
79	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
80	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
81	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
82	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
83	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
84	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
85	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
86	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
87	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
88	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
89	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
90	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
91	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162
92	67	1.1	657	18	T68111	H. p101 GPO 162	H. p101 GPO 162

us-09-410-835-4.011g.mrg

Page 4

0Y	1235	gtttctcttcacaaataaagctaaactctaaagctctaaagcgaagaagaaagaa	179
0Y	1201	gaattcttcacaaataaagctaaactctaaagctctaaagcgaagaagaaagaa	180
0Y	1199	ctctgaactctgaattaaagctctaaagctctaaagctctaaagcgaagaagaa	181
Db	1261	ctcgaacacgaatactaaagctctaaagcgaagaagcctctaaagcgaagaag	182
0Y	1855	atataacgattctggtttctctaaagcgaagaagcgaagaagcgaagaag	191
Db	1321	aagaacgctctgctctgtctctctaaagcgaagaagcgaagaagcgaagaag	198
0Y	1915	cttggatctaaaggaatttgagctaaactctaaagctctaaagctctaaagct	197
Db	1381	cttggatctaaaggaatttgagctaaactctaaagctctaaagctctaaagct	204
0Y	1975	tctgaacgaagaataaagctctaaactctaaagctctaaagctctaaagct	203
Db	1441	tctgaacgaagaataaagctctaaactctaaagctctaaagctctaaagct	210
0Y	2035	gttgatctctcaattctaaacacacacacacacacacacacacacacacac	209
Db	1501	gttgatctctcaattctaaacacacacacacacacacacacacacacacac	216
0Y	2095	gttcgaatctgggtctccctctctaaagctctaaagctctaaagctctaaag	215
Db	1561	gttcgaatctgggtctccctctctaaagctctaaagctctaaagctctaaag	222
0Y	2155	cctgaattctaaactctctgaactctctgaactctctgaactctctgaact	221
Db	1621	cctgaattctaaactctctgaactctctgaactctctgaactctctgaact	228
0Y	2215	acgcctaaagaatctgcgcgaacacacacacacacacacacacacacacac	227
Db	1681	acgcctaaagaatctgcgcgaacacacacacacacacacacacacacacac	234
0Y	2275	acacgaataatctgcgaataatctctctctaaagctctaaagctctaaag	233
Db	1741	acacgaataatctgcgaataatctctctctaaagctctaaagctctaaag	240
0Y	2315	acacgaataatctgcgaataatctctctctaaagctctaaagctctaaag	239
Db	1801	acacgaataatctgcgaataatctctctctaaagctctaaagctctaaag	246
0Y	2395	cgaagaatctctgaagaatctctgaagaatctctgaagaatctctgaaga	245
Db	1861	cgaagaatctctgaagaatctctgaagaatctctgaagaatctctgaaga	252
0Y	2455	aaatctgaacaaagctcgaactacacacacacacacacacacacacacac	251

Tue Mar 27 09:32:17 2001

us-09-410-035-4.011g.rng

Page 47

Tue Mar 27 09:32:17 2001

[illegible]

Tue Mar 27 09:32:17 2001

us-09-410-835-4.0149.rpt

Page 18

DT	RESULT 4
DE	V73601 standard; DNA: 449 BP.
CC	V73601:
CC	22-MAR-2000 (first entry)
CC	H. pylori cagA DNA fragment AM521001C2.
CC	PCR primer: probe: vacA_cagA; detection: vacuolating toxin; VDC;
CC	specificity: determinant gene: cytotoxin-associated gene; allele-specific
CC	infectivity: adhesion: mucosa-associated lymphoid tissue lymphoma; therapy:
CC	adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy:
CC	S region; S1a: S1b; S1c: S2; M region; M1; M2; ss.
CC	Helicobacter pylori.
CC	NO9816656-N2.
CC	21-MAR-1998.
CC	10-OCT-1997; 97NC-E005614.
CC	16-OCT-1995; 95EP-0070113.
CC	09-SEP-1997; 97EP-0070123.
CC	(11NC-) INNOGENETICS NV.
CC	(DDLC-) DDL BV.
CC	Quint W, Van Doorn L.
CC	WPI: 1998-351300/22.
CC	Method for detection and/or typing Helicobacter Pylori strain -
CC	comprise use of primer and probe based on vacA and cagA gene
CC	Claim 18; Figure 10: 123bp; English.
CC	This invention describes a novel method for the detection and/or typing
CC	of Helicobacter Pylori strain present in a sample using PCR primers a
CC	primers to detect regions of the vacuolating toxin (vacA) gene and other a
CC	gene. The method allows the typing and allele-specific detection (cagA)
CC	strain according to the VDC alleles present in that particular H. pylori
CC	strain. The vacuolating determinant genes are the genetic elements invol
CC	pathogenicity of the H. pylori strain. The method provides a way of
CC	detecting H. pylori strains in a sample with respect to the developmen
CC	of chronic active gastritis, gastric and duodenal ulcers, gastric

AC 714052.
D7
D8 09-SEP-1996 (first entry)
D9 Helicobacter pylori TagA DNA encoding a 96 KD antigenic fragment.
EM Antigen; Peptic ulcer; chronic gastritis; gastric adenocarcinoma;
FN diagnosis: predisposition; antibody: vaccine; infection; da.
X0
X1
X2 Helicobacter pylori.
X3
X4
X5
X6
X7 Key Location/Qualifiers
X8 CDS 1-368
X9 /tag a
X0 /1..1071
X1 5'UTR /tag b
X2
X3
X4 WD0610639-A2.
X5
X6 11-APR-1996.
X7
X8 29-SEP-1995; 5950-0012669.
X9
X0 30-SEP-1994; 9405-0316397.
X1
X2 (ORF-) GARYUX HPC
X3 (UTVA-) DNTV VANDERBILT.
X4
X5
X6
X7 Blaser M, Cover T, Kleinhous H, Tummuu MR.
X8 WPI: 1996-209561/71.
X9 P-PSDB: R91308.
X0
X1
X2 Helicobacter pylori Tag A gene - used to develop prods. for the
X3 carcinoma, treatment and prevention of peptic ulceration and gastric
X4 carcinoma
X5
X6 Claim 5: Page 88-93; 1189P: English.
X7
X8 714052 encodes a 96 KD antigenic fragment of the Helicobacter pylori
X9 (HP) TagA antigen. TagA, or its fragments, can be used to determine
X0 a predisposition to peptic ulceration or gastric carcinoma, both
X1 conditions caused by or linked to HP infection. TagA and its
X2 fragments can be used to detect HP infection. TagA antibodies or
X3 other ligands may also be used to treat peptic ulceration or gastric
X4 carcinoma caused by HP infection. TagA or a non-functional TagA
X5 gene may be used in vaccines for preventing and treating HP
X6 infection.
X7
X8
X9
X0 Sequence 1648 BP: 1296 A: 660 C: 692 G: 998 T: 0 other:

16-OCT-1996: 96EP-0870131.
 09-SEP-1997: 97EP-0870133.
 PA (INNO-) INNOGENETICS NV.
 PA (DDLD-) DDL BV.
 PA Quint W., Van Doorn L.
 PI: 1998-251300/22.
 DR WPI: 1998-251300/22.

Method for detecting and/or typing Helicobacter pylori strains
 comprises use of primers and probes based on vacA and cagA gene
 Claim 18: Figure 10: 12bp: English.

This invention describes a novel method for the detection and/or typing of Helicobacter pylori strains present in a sample using PCR primers and probes to detect regions of the vacuolating toxin (vacA) gene and other virulence determinant genes (VDC) e.g. the cytotoxin-associated (cagA) gene. The method allows the typing and allele-specific detection of a strain according to the VDC alleles present in that particular H. pylori strain. The method also allows the detection of the genetic elements involved in enabling, determining, and marking the infectivity and/or pathogenicity of the H. pylori strain. The method provides a way of detecting H. pylori strains in a sample with respect to the development of chronic active gastritis, gastric and duodenal ulcers, gastric adenocarcinoma, mucosa-associated lymphoid tissue (MALT) lymphoma, and/or determining eradication therapy. V73508-V73546 represent PCR primers and probes used in the detection of the H. pylori vacA and cagA genes. The primers and probes are used especially to detect the vacA S regions V73547-V73785.

Sequence 449 BP: 162 A: 96 C: 72 G: 119 T: 0 other:
 Query Match 3.0% Score 179: DB 19: Length 449:
 Best Local Similarity 99.1% Pred. No. 1.1e-66:
 Matches 329: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

652 gattccgataaataacacatcgttataaagaagagagatagacagacatttga 711
 118 gattccgataaataacacatcgttataaagaagagagatagacagacatttga 177
 712 gattccgataaataacacatcgttataaagaagagagatagacagacatttga 771
 178 gattccgataaataacacatcgttataaagaagagagatagacagacatttga 237
 772 gattccgataaataacacatcgttataaagaagagagatagacagacatttga 831
 238 gattccgataaataacacatcgttataaagaagagagatagacagacatttga 297

Tue Mar 27 09:32:17 2001

us-09-410-835-4.o11g.mg

Page 67

Claim 18: Figure 10: 12bp: English.

This invention describes a novel method for the detection and/or typing of Helicobacter pylori strains present in a sample using PCR primers and probes to detect regions of the vacuolating toxin (vacA) gene and other virulence determinant genes (VDC) e.g. the cytotoxin-associated (cagA) gene. The method allows the typing and allele-specific detection of a strain according to the VDC alleles present in that particular H. pylori strain. The method also allows the detection of the genetic elements involved in enabling, determining, and marking the infectivity and/or pathogenicity of the H. pylori strain. The method provides a way of detecting H. pylori strains in a sample with respect to the development of chronic active gastritis, gastric and duodenal ulcers, gastric adenocarcinoma, mucosa-associated lymphoid tissue (MALT) lymphoma, and/or determining eradication therapy. V73508-V73546 represent PCR primers and probes used in the detection of the H. pylori vacA and cagA genes. The primers and probes are used especially to detect the vacA S regions V73547-V73785.

Sequence 449 BP: 164 A: 96 C: 71 G: 118 T: 0 other:

Query Match 3.0% Score 179: DB 19: Length 449:
 Best Local Similarity 99.1% Pred. No. 1.1e-66:
 Matches 329: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

652 gattccgataaataacacatcgttataaagaagagagatagacagacatttga 711
 118 gattccgataaataacacatcgttataaagaagagagatagacagacatttga 177
 712 gattccgataaataacacatcgttataaagaagagagatagacagacatttga 771
 178 gattccgataaataacacatcgttataaagaagagagatagacagacatttga 237
 772 gattccgataaataacacatcgttataaagaagagagatagacagacatttga 831
 238 gattccgataaataacacatcgttataaagaagagagatagacagacatttga 297
 832 attgattgataatcttcacaaagagcttcgaatttggagatcagcttaccgaatt 891
 298 attgattgataatcttcacaaagagcttcgaatttggagatcagcttaccgaatt 357
 892 ttccaaagtgggtgtccatcaaaagcttcgaatttggagatcagcttaccgaatt 951
 358 ttccaaagtgggtgtccatcaaaagcttcgaatttggagatcagcttaccgaatt 417
 952 attttatgaaatcttcacaaagagcttcgaatttggagatcagcttaccgaatt 479
 418 attttatgaaatcttcacaaagagcttcgaatttggagatcagcttaccgaatt 449

Tue Mar 27 09:32:17 2001

us-09-410-835-4.o11g.mg

Page 66

812 attgattgataatcttcacaaagagcttcgaatttggagatcagcttaccgaatt 891
 298 attgattgataatcttcacaaagagcttcgaatttggagatcagcttaccgaatt 357
 892 ttccaaagtgggtgtccatcaaaagcttcgaatttggagatcagcttaccgaatt 951
 358 ttccaaagtgggtgtccatcaaaagcttcgaatttggagatcagcttaccgaatt 417
 952 attttatgaaatcttcacaaagagcttcgaatttggagatcagcttaccgaatt 479
 418 attttatgaaatcttcacaaagagcttcgaatttggagatcagcttaccgaatt 449

RESULT 15

ID V73611 standard: DNA: 449 BP.

XC V73611:

DT 22-APR-2000 (first entry)

DE H. pylori cagA DNA fragment M82001C2.

XX PCR primer: probe: vacA: cagA: detection: vacuolating toxin; VDC:

XX virulence determinant gene: cytotoxin-associated (cagA) gene and other

XX infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;

XX adenocarcinoma; mucosa-associated lymphoid tissue (MALT) lymphoma; therapy;

XX S region: S1; S1b; S1c; S2; M region: M1; M2; M3.

OS Helicobacter pylori.

XX M091658-A2.

XX 23-APR-1998.

PP 16-OCT-1997: 97NO-EP05614.

XX 16-OCT-1996: 96EP-0870131.

PR 09-SEP-1997: 97EP-0870133.

PA (INNO-) INNOGENETICS NV.

PA (DDLD-) DDL BV.

PI Quint W., Van Doorn L.

DR WPI: 1998-251300/22.

Method for detecting and/or typing Helicobacter pylori strains
 comprises use of primers and probes based on vacA and cagA gene

Tue Mar 27 09:32:17 2001

us-09-410-835-4.o11g.mg

Page 68

RESULT 16

ID V73604 standard: DNA: 449 BP.

XC V73604:

DT 22-MAR-2000 (first entry)

DE H. pylori cagA DNA fragment M845001C2.

XX PCR primer: probe: vacA: cagA: detection: vacuolating toxin; VDC:

XX virulence determinant gene: cytotoxin-associated (cagA) gene and other

XX infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;

XX adenocarcinoma; mucosa-associated lymphoid tissue (MALT) lymphoma; therapy;

XX S region: S1; S1b; S1c; S2; M region: M1; M2; M3.

OS Helicobacter pylori.

XX M091658-A2.

XX 23-APR-1998.

PP 16-OCT-1997: 97NO-EP05614.

XX 16-OCT-1996: 96EP-0870131.

PR 09-SEP-1997: 97EP-0870133.

PA (INNO-) INNOGENETICS NV.

PA (DDLD-) DDL BV.

PI Quint W., Van Doorn L.

DR WPI: 1998-251300/22.

Method for detecting and/or typing Helicobacter pylori strains
 comprises use of primers and probes based on vacA and cagA gene

This invention describes a novel method for the detection and/or typing of Helicobacter pylori strains present in a sample using PCR primers and probes to detect regions of the vacuolating toxin (vacA) gene and other virulence determinant genes (VDC) e.g. the cytotoxin-associated (cagA) gene. The method allows the typing and allele-specific detection of a strain according to the VDC alleles present in that particular H. pylori strain. The method also allows the detection of the genetic elements involved in enabling, determining, and marking the infectivity and/or pathogenicity of the H. pylori strain. The method provides a way of detecting H. pylori strains in a sample with respect to the development of chronic active gastritis, gastric and duodenal ulcers, gastric

Tue Mar 27 09:12:17 2001

us-09-410-835-4.011g.png

Page 75

Tue Mar 27 09:32:17 2001

us-09-610-035-4.011g.km

Page 76

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.rng

Page 83

00-410-035 4-11-

Query Match	1.99;	Score 110;	DB 20;	Length 285;
Best Local Similarity	100.0%;	Pred. No. 2.5e-37;		
Matches 110;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Db	Sequence	Position
226	TCAGCTTACCGAATTTTCAGCTGCTGCTCCATMAACGATCGCTMAATCA	16
936	CACCGATCGATCGGAATTTATGAGAAATATCATACACCCCTATCC	985

LD 100 CACCACATCATCCGAAATTATGCAAAATATCATCATCAACCCGCTATCC 117

RESULT 26

unref:0

XX 18-FTM-1000 (41-58-224-22)

Tue Mar 27 09:32:17 2001
 us-09-410-035-4.colli.rmg
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC V13547-V13785.
 XX
 50 Sequence 449 BP: 165 A; 98 C; 70 G; 116 T; 0 other:

Tue May 27 09:32:17 2001

00-410-035 4-11-

CC that is characterised by immunoreactivity with *H. pylori*-positive
CC antisera. The proteins are highly immunogenic and induce a long-lasting
CC immune response that persists even after antimicrobial treatment. In
CC antibody-detection assays, on sera, plasma, urine, saliva etc., they

CC previously unrecognised immunogenic cluster families. *H. pylori* antigens
CC are used to detect *H. pylori*-specific antibodies, for diagnosing
CC infection or to confirm eradication of infection, and in vaccines to
CC protect against *H. pylori* infection and related diseases (gastritis,

Seq Sequence 2705 BP; 942 A; 490 C; 469 G; 804 T; 0 other;
Query Match 1 08. Score 110. 20 20. 100.00

Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 876 tcagcgttaccgaatttcacaaagttggtgtcccatcaaaagatcgtctaaatcaa 935

CC pathogenicity of the H. pylori strain. The method provides a way of
CC detecting H. pylori strains in a sample with respect to the development
CC of ulcers, gastric and duodenal ulcers, gastric
CC adenocarcinoma, mucosa-associated lymphoid tissue lymphoma; therapy;
CC determining eradication therapy. V73508-V73546 represent PCR primers
CC and probes used in the detection of the H. pylori vacA and cagA genes.
CC The primers and probes are used especially to detect the vacA S regions
CC S1a/S2 and the M regions M1 and M2 which are represented in
CC V73547-V73785.

50 Sequence 464 BP: 177 A: 93 C: 69 G: 125 T: 0 other:

Query Match 0.84; Score 49; DB 19; Length 464;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Or 764 ccaaaagacgcagatcttcagacttcacataagacagatgatt 812
Db 245 ccaaaagacgcagatcttcagacttcacataagacagatgatt 293

RESULT 36
V73617
ID V73617 standard: DNA: 464 BP.
XX V73617;
XX 22-MAR-2000 (first entry)

XX H. pylori cagA DNA fragment BM12001C2.
XX
XX PCR primer: probe: vacA: cagA: detection: vacuolating toxin: VDC:
XX virulence determinant gene: cytotoxin-associated gene: allele-specific:
XX infectivity: pathogenicity: gastritis: gastric: duodenal: ulcer:
XX adenocarcinoma: mucosa-associated lymphoid tissue lymphoma: therapy:
XX S region: S1a; S1b; S1c; S2; M region: M1; M2; M3.

XX Helicobacter pylori.
XX
XX M0981658-A2.
XX
XX 23-APR-1998.
XX
XX 10-OCT-1997: 97MO-EP05614.
XX
XX 16-OCT-1996: 96EP-0870131.
XX
XX 09-SEP-1997: 97EP-0870133.
XX
XX (JNNO-) INNOCENTICS NV.
XX (DDLD-) DDL BV.

XX Quint W. Van Doorn L.
XX
XX WPI: 1998-251300/22.
XX
XX Method for detecting and/or typing Helicobacter pylori strains -
XX comprises use of primers and probes based on vacA and cagA gene

XX Claim 18: Figure 10: 122pp: English.

XX This invention describes a novel method for the detection and/or typing
XX of Helicobacter pylori strains present in a sample using PCR primers and
XX probes to detect regions of the vacuolating toxin (vacA) gene and other
XX genes. The method allows the typing and allele-specific detection of a
XX strain according to the VDC alleles present in that particular H. pylori
XX strain. The virulence determinant genes are the genetic elements involved
XX in enabling, determining, and marking the infectivity and/or
XX detecting H. pylori strains in a sample with respect to the development
XX of chronic active gastritis, gastric and duodenal ulcers, gastric
XX adenocarcinoma, mucosa-associated lymphoid tissue lymphoma, and/or
XX determining eradication therapy. V73508-V73546 represent PCR primers
XX and probes used in the detection of the H. pylori vacA and cagA genes.
XX S1a/S2 and S2 and the M regions M1 and M2 which are represented in
XX V73547-V73785.

50 Sequence 464 BP: 177 A: 93 C: 69 G: 125 T: 0 other:

Thu Mar 27 09:32:17 2001

us-09-410-835-4-0119.rmg

Page 99

KM virulence determinant gene: cytotoxin-associated gene: allele-specific:
KM infectivity: pathogenicity: gastritis: gastric: duodenal: ulcer:
KM adenocarcinoma: mucosa-associated lymphoid tissue lymphoma: therapy;
KM S region: S1a; S1b; S1c; S2; M region: M1; M2; M3.

XX Helicobacter pylori.
XX
XX M0981658-A2.
XX
XX 23-APR-1998.
XX
XX 10-OCT-1997: 97MO-EP05614.
XX
XX 16-OCT-1996: 96EP-0870131.
XX
XX 09-SEP-1997: 97EP-0870133.
XX
XX (JNNO-) INNOCENTICS NV.
XX (DDLD-) DDL BV.

XX Quint W. Van Doorn L.
XX
XX WPI: 1998-251300/22.
XX
XX Method for detecting and/or typing Helicobacter pylori strains -
XX comprises use of primers and probes based on vacA and cagA gene

XX Claim 18: Figure 10: 122pp: English.

XX This invention describes a novel method for the detection and/or typing
XX of Helicobacter pylori strains present in a sample using PCR primers and
XX probes to detect regions of the vacuolating toxin (vacA) gene and other
XX genes. The method allows the typing and allele-specific detection of a
XX strain according to the VDC alleles present in that particular H. pylori
XX strain. The virulence determinant genes are the genetic elements involved
XX in enabling, determining, and marking the infectivity and/or
XX detecting H. pylori strains in a sample with respect to the development
XX of chronic active gastritis, gastric and duodenal ulcers, gastric
XX adenocarcinoma, mucosa-associated lymphoid tissue lymphoma, and/or
XX determining eradication therapy. V73508-V73546 represent PCR primers
XX and probes used in the detection of the H. pylori vacA and cagA genes.
XX S1a/S2 and S2 and the M regions M1 and M2 which are represented in
XX V73547-V73785.

50 Sequence 464 BP: 177 A: 93 C: 69 G: 125 T: 0 other:

Query Match 0.84; Score 49; DB 19; Length 464;
Best Local Similarity 100.0%; Pred. No. 2e-11;

XX
XX Quint W. Van Doorn L.
XX
XX WPI: 1998-251300/22.
XX
XX Method for detecting and/or typing Helicobacter pylori strains -
XX comprises use of primers and probes based on vacA and cagA gene

XX Claim 18: Figure 10: 122pp: English.

XX This invention describes a novel method for the detection and/or typing
XX of Helicobacter pylori strains present in a sample using PCR primers and
XX probes to detect regions of the vacuolating toxin (vacA) gene and other
XX genes. The method allows the typing and allele-specific detection of a
XX strain according to the VDC alleles present in that particular H. pylori
XX strain. The virulence determinant genes are the genetic elements involved
XX in enabling, determining, and marking the infectivity and/or
XX detecting H. pylori strains in a sample with respect to the development
XX of chronic active gastritis, gastric and duodenal ulcers, gastric
XX adenocarcinoma, mucosa-associated lymphoid tissue lymphoma, and/or
XX determining eradication therapy. V73508-V73546 represent PCR primers
XX and probes used in the detection of the H. pylori vacA and cagA genes.
XX S1a/S2 and S2 and the M regions M1 and M2 which are represented in
XX V73547-V73785.

50 Sequence 464 BP: 177 A: 93 C: 69 G: 125 T: 0 other:

Query Match 0.84; Score 49; DB 19; Length 464;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Or 764 ccaaaagacgcagatcttcagacttcacataagacagatgatt 812
Db 245 ccaaaagacgcagatcttcagacttcacataagacagatgatt 293

RESULT 37
V73620
ID V73620 standard: DNA: 464 BP.
XX V73620;
XX 22-MAR-2000 (first entry)

XX H. pylori cagA DNA fragment CH4001C2.
XX
XX PCR primer: probe: vacA: cagA: detection: vacuolating toxin: VDC:
XX virulence determinant gene: cytotoxin-associated gene: allele-specific:
XX infectivity: pathogenicity: gastritis: gastric: duodenal: ulcer:
XX adenocarcinoma: mucosa-associated lymphoid tissue lymphoma: therapy:
XX S region: S1a; S1b; S1c; S2; M region: M1; M2; M3.

XX Helicobacter pylori.
XX
XX M0981658-A2.
XX
XX 23-APR-1998.
XX
XX 10-OCT-1997: 97MO-EP05614.
XX
XX 16-OCT-1996: 96EP-0870131.
XX
XX 09-SEP-1997: 97EP-0870133.
XX
XX (JNNO-) INNOCENTICS NV.
XX (DDLD-) DDL BV.

XX Quint W. Van Doorn L.
XX
XX WPI: 1998-251300/22.
XX
XX Method for detecting and/or typing Helicobacter pylori strains -
XX comprises use of primers and probes based on vacA and cagA gene

XX Claim 18: Figure 10: 122pp: English.

XX This invention describes a novel method for the detection and/or typing
XX of Helicobacter pylori strains present in a sample using PCR primers and
XX probes to detect regions of the vacuolating toxin (vacA) gene and other
XX genes. The method allows the typing and allele-specific detection of a
XX strain according to the VDC alleles present in that particular H. pylori
XX strain. The virulence determinant genes are the genetic elements involved
XX in enabling, determining, and marking the infectivity and/or
XX detecting H. pylori strains in a sample with respect to the development
XX of chronic active gastritis, gastric and duodenal ulcers, gastric
XX adenocarcinoma, mucosa-associated lymphoid tissue lymphoma, and/or
XX determining eradication therapy. V73508-V73546 represent PCR primers
XX and probes used in the detection of the H. pylori vacA and cagA genes.
XX S1a/S2 and S2 and the M regions M1 and M2 which are represented in
XX V73547-V73785.

Thu Mar 27 09:32:17 2001

us-09-410-835-4-0119.rmg

Page 100

KM virulence determinant gene: cytotoxin-associated gene: allele-specific:
KM infectivity: pathogenicity: gastritis: gastric: duodenal: ulcer:
KM adenocarcinoma: mucosa-associated lymphoid tissue lymphoma: therapy;
KM S region: S1a; S1b; S1c; S2; M region: M1; M2; M3.

XX Helicobacter pylori.
XX
XX M0981658-A2.
XX
XX 23-APR-1998.
XX
XX 10-OCT-1997: 97MO-EP05614.
XX
XX 16-OCT-1996: 96EP-0870131.
XX
XX 09-SEP-1997: 97EP-0870133.
XX
XX (JNNO-) INNOCENTICS NV.
XX (DDLD-) DDL BV.

XX Quint W. Van Doorn L.
XX
XX WPI: 1998-251300/22.
XX
XX Method for detecting and/or typing Helicobacter pylori strains -
XX comprises use of primers and probes based on vacA and cagA gene

XX Claim 18: Figure 10: 122pp: English.

XX This invention describes a novel method for the detection and/or typing
XX of Helicobacter pylori strains present in a sample using PCR primers and
XX probes to detect regions of the vacuolating toxin (vacA) gene and other
XX genes. The method allows the typing and allele-specific detection of a
XX strain according to the VDC alleles present in that particular H. pylori
XX strain. The virulence determinant genes are the genetic elements involved
XX in enabling, determining, and marking the infectivity and/or
XX detecting H. pylori strains in a sample with respect to the development
XX of chronic active gastritis, gastric and duodenal ulcers, gastric
XX adenocarcinoma, mucosa-associated lymphoid tissue lymphoma, and/or
XX determining eradication therapy. V73508-V73546 represent PCR primers
XX and probes used in the detection of the H. pylori vacA and cagA genes.
XX S1a/S2 and S2 and the M regions M1 and M2 which are represented in
XX V73547-V73785.

50 Sequence 464 BP: 177 A: 93 C: 69 G: 125 T: 0 other:

[illegible]

Query Match	0.4%	Score 25:	DB 19:	Length 28:
NCBI Local Statistics	100.0%	Prod No. 0.4:		
Matches	25:	Conservative	0:	Mismatches
			0:	Indels
			0:	Gaps
1016	ttcccaaaagaccctcagcctctc	1840		
DB	35	ttcccaaaagaccctcagcctctc	1	
RESULT 46				
250142/C				
XX	250142 standard: DNA: 34 BP.			
AC	250142:			
XX				
XX	04-MAY-2000 (first entry)			
DT				
DE	CAG 2 PCR primer for H. pylori GGT gene amplification.			
XX				
XX	PCR primer: gamma-glutamyl transpeptidase: GGT: antibody: vaccine:			
XX	Helicobacter Infection: chronic gastritis: gastroduodenal ulcer:			
XX	Gastric cancer: probe: antibacterial: anticler: antiinflammatory:			
XX	cytotoxin: ds.			
XX	Helicobacter pylori.			
XX				
XX	NC020001031-91.			
XX				
PD	13-JAN-2000.			
XX				
XX	28-JUN-1999: 99MC-EP04459.			
PP				
XX	01-JUL-1999: 98US-0100213.			
PR				
XX	(1NSP) INST PASTERU.			
PA				
XX	Chevalier C, Thibierge J, Labigne A:			
XX				
XX	WPI: 2000-182116/16.			
DR				
XX	New isolated bacterial enzymes used to develop products for the			
XX	detection and treatment of Helicobacter Infections.			
P7	particularity H. pylori Infections.			
XX				
P5	Example 1: Page 32: 96P: English.			
XX				
XX	The patent discloses the use of a purified polynucleotide coding for			
CC	gamma-glutamyl transpeptidase (GGT) from Helicobacter pylori			
XX	antibodies induced by the corresponding protein can be used for			
XX	detecting Helicobacter Infection, particularly H. pylori. The			

PT Method for detecting and/or typing *Helicobacter pylori* strains
PT comprises use of primers and probes based on vacA and cagA gene
XX
XX
XX Claim 1: Page 44; 122pp. English.
CC This invention describes a novel method for the detection and/or typing
CC of *Helicobacter pylori* strains present in a sample using PCR primers and
CC probes to detect regions of the Vacuolating toxin (*vacA*) gene and other
CC genes. The method also employs the use of a specific primer associated (cagA)
CC strain. The method allows the typing of at least one *H. pylori*
CC strain according to the VGC alleles present in that particular *H. pylori*
CC strain. The virulence determinant genes are the genetic elements involved
CC pathogenically determining, and marking the infectivity and/or
CC detecting *H. pylori* strains in a sample with respect to the development
CC of chronic active gastritis, gastric and duodenal ulcers, gastric
CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas; and/or
CC cancer. The method also includes the use of a specific primer associated
CC and probes used in the detection of the *H. pylori* strains.
CC The primers and probes are used especially to detect the *vacA*'s regions
CC 61A/b/c and g2 and the M regions M1 and M2 which are represented in
XX sequence VJ3549-VJ3780.
SQ Sequence 24 BP; 11 A; 8 C; 3 G; 2 T; 0 other;
Query Match 0.4%; Score 24; DB 19; Length 24;
Best Local Similarity 100.0%; Pval No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0
DY 551 ttgcaccatcaccaaacccaacgaag 574
DB 1 ttgcaccatcaccaaacccaacgaag 24
PROBUT 48
V45504/C
ID V45504 standard; DNA; 30 BP.
XX
XX V45504:
D7 15-FPM-1999 (first entry)
XX
XX Helicobacter pylori cagA gene PCR primer:
XX
XX Vaccine: antigen; antigen; toxin; diagnosis; gastritis; ulcer;
RV stomach cancer; caga gene; PCR; primer; ss.
XX
XX Synthetic.
XX Helicobacter pylori.

```

X1  M09844310-AL.
X2  08-OCT-1998.
X3
X4  31-MAR-1998. 98MO-R800073.
X5
X6  31-MAR-1997. 97FE-0011851.
X7  31-MAR-1997. 97FE-0011850.
X8
X9  (DAEM-) DAEMOONG PHARM CO LTD.
X10
X11  Choi D., Jung H., Kim B., Park M., Shin S., Yu Y;
X12  WPI: 1998-568279/48.
X13
X14  New chimeric protein for use against Helicobacter pylori -
X15  comprising an antigenic protein of H. pylori and subunits
X16  of Vibrio cholerae toxin, preferably produced by recombinant
X17  techniques
X18
X19  Example 2-2: Page 10, 102pp; English.
X20
X21  PCR primers (see V45503 and V45504) are designed for the PCR
X22  application of the Helicobacter pylori cagA gene. The invention
X23  comprises a method for identifying a mutation comprising a cagA
X24  gene) by ligating an antigenic determinant consisting a cagA
X25  gene) of H. pylori and A2 and B subunit genes of Vibrio 9, the
X26  cholerae. Also claimed are chimeric proteins (see W80599-600)
X27  comprising a recombinant protein, methods for the recombinant
X28  production of the chimeric proteins, and vaccines for the
X29  prevention of the disease, and therapeutic vaccines for H. pylori-
X30  associated diseases such as gastritis, gastric ulcer, duodenal
X31  ulcer and gastric cancer.
X32
X33  Sequence 30 BP; 10 A.; 5 C.; 4 G.; 11 T.; 0 other:
X34
X35
X36
X37
X38
X39
X40
X41
X42
X43
X44
X45
X46
X47
X48
X49
X50
X51
X52
X53
X54
X55
X56
X57
X58
X59
X60
X61
X62
X63
X64
X65
X66
X67
X68
X69
X70
X71
X72
X73
X74
X75
X76
X77
X78
X79
X80
X81
X82
X83
X84
X85
X86
X87
X88
X89
X90
X91
X92
X93
X94
X95
X96
X97
X98
X99
1000

```

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.rng

Page 115

AC	X145322	
AD	31-MAR-1999	(first entry)
AE		
DE	H. pylori OMHO 1302 gene.	
DD		
CC	CMO protein, Helicobacter infection, gastroduodenal disease, gastritis,	
BN	peptic ulcer disease, ss.	
OS	Helicobacter pylori.	
PH	Key	Location/Qualifiers
FT	CDS	91..2448
FT		/tag= a
PD	MO984378-AL.	
PD	08-OCT-1998.	
PD	01-APR-1998.	98NM-006037.1.
PD		
PD	28-JUL-1997.	97US-0902615.
PR	01-APR-1997.	97US-0831457.
PR	24-JUN-1997.	97US-0881277.
PA	(HDA)- HUMAN GENOME SCI INC.	
PA	110MR. MERCKUS ORMAVA PASTER MERCKUS SERUMS.	
PI	Al-Caravi M, Kleanthous H, Miller C, Oomen RP, Tomb J,	
PI	WPI: 1998-542293/46.	
PI	P-PSDB01 980603.	
PT	New isolated Helicobacter polynucleotides - used to develop products	
PT	for the diagnosis, prevention and treatment of Helicobacter	
XX	Infections and gastrointestanal diseases	
XX	Claim 1: Page 1757-1761. 205kbp. English.	
XX		
XX	This sequence represents a polynucleotide of the invention. It was	
XX	sequenced from a Helicobacter pylori CMO protein.	
XX	The polypeptides can be used for preventing or treating Helicobacter	
XX	Infections, including acute, chronic, and atrophic gastritis, and peptic	
XX	ulcers, and duodenal ulcers. They can also be used	
XX	for the production of antibodies. The products can also be used for	
XX	detection and diagnosis.	
XX	Sequence 2459 BP: 806 A: 455 C: 596 G: 641 T: 0 other:	

Tue Mar 27 09:32:17 2001

us-09-410-835-4.01lg.rng

Page 116

PA (GENE-) GENERALS TECHNOLOGIES INC.

PI Chow TP, Fry KE, Lim WY, McAtee CP.

XX WPI: 1999-009433/01.

DR New Helicobacter pylori antigens and related nucleic acid sequences
PT - useful in serological diagnosis and protective vaccines, providing
XX long-lasting immune response

XX Claim 27: Page 144: 402pp: English.

CC The present sequence encodes a Helicobacter pylori antigenic protein
CC that is characterized by immunoreactivity with H. pylori-positive
CC antisera. The protein is highly immunogenic and induce a long-lasting
CC antibody response even after antimicrobial treatment. In
CC addition, the protein is highly immunogenic and induce a long-lasting
CC antibody response even after antimicrobial treatment. They are
CC highly sensitive and specific. The specification also describes a
CC previously unrecognized immunogenic cluster families. H. pylori antigens
CC are used to detect H. pylori-specific antibodies, for diagnosing
CC infection, confirm eradication of infection, and in vaccines to
CC protect against H. pylori infection and related diseases (gastritis,
CC peptic ulcer, gastric adenocarcinoma/lymphoma).

SQ Sequence 267 BP: 101 A; 39 C; 31 G; 94 T; 0 other:

Query Match 0.44; Score 21; DB 20; Length 267;

Best Local Similarity 100.0%; Pred. No. 6.3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 427 atgtctcaaacagatgata 448

DB 238 atgtctcaaacagatgata 259

RESULT 53

V73577/C

ID V73577 standard: DNA; 21 BP.

AC V73577;

XX 22-MAR-2000 (first entry)

XX H. pylori cag A primer: cagSR.

XX PCR primer: probe: vacA; cagA; detection: vacuolating toxin; VDC:

XX virulence determinant gene; cytotoxin-associated gene; allele-specific;

XX adenocarcinoma; gastritis; gastric; duodenal; ulcer;

XX adenocarcinoma; gastritis; gastric; duodenal; ulcer;

XX S region; S1A; S1B; S1C; S2; M region; M1; M2; M3; M4; M5; M6; M7; M8; M9; M10; M11; M12; M13; M14; M15; M16; M17; M18; M19; M20; M21; M22; M23; M24; M25; M26; M27; M28; M29; M30; M31; M32; M33; M34; M35; M36; M37; M38; M39; M40; M41; M42; M43; M44; M45; M46; M47; M48; M49; M50; M51; M52; M53; M54; M55; M56; M57; M58; M59; M60; M61; M62; M63; M64; M65; M66; M67; M68; M69; M70; M71; M72; M73; M74; M75; M76; M77; M78; M79; M80; M81; M82; M83; M84; M85; M86; M87; M88; M89; M90; M91; M92; M93; M94; M95; M96; M97; M98; M99; M100; M101; M102; M103; M104; M105; M106; M107; M108; M109; M110; M111; M112; M113; M114; M115; M116; M117; M118; M119; M120; M121; M122; M123; M124; M125; M126; M127; M128; M129; M130; M131; M132; M133; M134; M135; M136; M137; M138; M139; M140; M141; M142; M143; M144; M145; M146; M147; M148; M149; M150; M151; M152; M153; M154; M155; M156; M157; M158; M159; M160; M161; M162; M163; M164; M165; M166; M167; M168; M169; M170; M171; M172; M173; M174; M175; M176; M177; M178; M179; M180; M181; M182; M183; M184; M185; M186; M187; M188; M189; M190; M191; M192; M193; M194; M195; M196; M197; M198; M199; M200; M201; M202; M203; M204; M205; M206; M207; M208; M209; M210; M211; M212; M213; M214; M215; M216; M217; M218; M219; M220; M221; M222; M223; M224; M225; M226; M227; M228; M229; M230; M231; M232; M233; M234; M235; M236; M237; M238; M239; M240; M241; M242; M243; M244; M245; M246; M247; M248; M249; M250; M251; M252; M253; M254; M255; M256; M257; M258; M259; M260; M261; M262; M263; M264; M265; M266; M267; M268; M269; M270; M271; M272; M273; M274; M275; M276; M277; M278; M279; M280; M281; M282; M283; M284; M285; M286; M287; M288; M289; M290; M291; M292; M293; M294; M295; M296; M297; M298; M299; M300; M301; M302; M303; M304; M305; M306; M307; M308; M309; M310; M311; M312; M313; M314; M315; M316; M317; M318; M319; M320; M321; M322; M323; M324; M325; M326; M327; M328; M329; M330; M331; M332; M333; M334; M335; M336; M337; M338; M339; M340; M341; M342; M343; M344; M345; M346; M347; M348; M349; M350; M351; M352; M353; M354; M355; M356; M357; M358; M359; M360; M361; M362; M363; M364; M365; M366; M367; M368; M369; M370; M371; M372; M373; M374; M375; M376; M377; M378; M379; M380; M381; M382; M383; M384; M385; M386; M387; M388; M389; M390; M391; M392; M393; M394; M395; M396; M397; M398; M399; M400; M401; M402; M403; M404; M405; M406; M407; M408; M409; M410; M411; M412; M413; M414; M415; M416; M417; M418; M419; M420; M421; M422; M423; M424; M425; M426; M427; M428; M429; M430; M431; M432; M433; M434; M435; M436; M437; M438; M439; M440; M441; M442; M443; M444; M445; M446; M447; M448; M449; M450; M451; M452; M453; M454; M455; M456; M457; M458; M459; M460; M461; M462; M463; M464; M465; M466; M467; M468; M469; M470; M471; M472; M473; M474; M475; M476; M477; M478; M479; M480; M481; M482; M483; M484; M485; M486; M487; M488; M489; M490; M491; M492; M493; M494; M495; M496; M497; M498; M499; M500; M501; M502; M503; M504; M505; M506; M507; M508; M509; M510; M511; M512; M513; M514; M515; M516; M517; M518; M519; M520; M521; M522; M523; M524; M525; M526; M527; M528; M529; M530; M531; M532; M533; M534; M535; M536; M537; M538; M539; M540; M541; M542; M543; M544; M545; M546; M547; M548; M549; M550; M551; M552; M553; M554; M555; M556; M557; M558; M559; M560; M561; M562; M563; M564; M565; M566; M567; M568; M569; M570; M571; M572; M573; M574; M575; M576; M577; M578; M579; M580; M581; M582; M583; M584; M585; M586; M587; M588; M589; M590; M591; M592; M593; M594; M595; M596; M597; M598; M599; M600; M601; M602; M603; M604; M605; M606; M607; M608; M609; M610; M611; M612; M613; M614; M615; M616; M617; M618; M619; M620; M621; M622; M623; M624; M625; M626; M627; M628; M629; M630; M631; M632; M633; M634; M635; M636; M637; M638; M639; M640; M641; M642; M643; M644; M645; M646; M647; M648; M649; M650; M651; M652; M653; M654; M655; M656; M657; M658; M659; M660; M661; M662; M663; M664; M665; M666; M667; M668; M669; M670; M671; M672; M673; M674; M675; M676; M677; M678; M679; M680; M681; M682; M683; M684; M685; M686; M687; M688; M689; M690; M691; M692; M693; M694; M695; M696; M697; M698; M699; M700; M701; M702; M703; M704; M705; M706; M707; M708; M709; M710; M711; M712; M713; M714; M715; M716; M717; M718; M719; M720; M721; M722; M723; M724; M725; M726; M727; M728; M729; M730; M731; M732; M733; M734; M735; M736; M737; M738; M739; M740; M741; M742; M743; M744; M745; M746; M747; M748; M749; M750; M751; M752; M753; M754; M755; M756; M757; M758; M759; M760; M761; M762; M763; M764; M765; M766; M767; M768; M769; M770; M771; M772; M773; M774; M775; M776; M777; M778; M779; M780; M781; M782; M783; M784; M785; M786; M787; M788; M789; M790; M791; M792; M793; M794; M795; M796; M797; M798; M799; M800; M801; M802; M803; M804; M805; M806; M807; M808; M809; M810; M811; M812; M813; M814; M815; M816; M817; M818; M819; M820; M821; M822; M823; M824; M825; M826; M827; M828; M829; M830; M831; M832; M833; M834; M835; M836; M837; M838; M839; M840; M841; M842; M843; M844; M845; M846; M847; M848; M849; M850; M851; M852; M853; M854; M855; M856; M857; M858; M859; M860; M861; M862; M863; M864; M865; M866; M867; M868; M869; M870; M871; M872; M873; M874; M875; M876; M877; M878; M879; M880; M881; M882; M883; M884; M885; M886; M887; M888; M889; M890; M891; M892; M893; M894; M895; M896; M897; M898; M899; M900; M901; M902; M903; M904; M905; M906; M907; M908; M909; M910; M911; M912; M913; M914; M915; M916; M917; M918; M919; M920; M921; M922; M923; M924; M925; M926; M927; M928; M929; M930; M931; M932; M933; M934; M935; M936; M937; M938; M939; M940; M941; M942; M943; M944; M945; M946; M947; M948; M949; M950; M951; M952; M953; M954; M955; M956; M957; M958; M959; M960; M961; M962; M963; M964; M965; M966; M967; M968; M969; M970; M971; M972; M973; M974; M975; M976; M977; M978; M979; M980; M981; M982; M983; M984; M985; M986; M987; M988; M989; M990; M991; M992; M993; M994; M995; M996; M997; M998; M999; M1000; M1001; M1002; M1003; M1004; M1005; M1006; M1007; M1008; M1009; M1010; M1011; M1012; M1013; M1014; M1015; M1016; M1017; M1018; M1019; M1020; M1021; M1022; M1023; M1024; M1025; M1026; M1027; M1028; M1029; M1030; M1031; M1032; M1033; M1034; M1035; M1036; M1037; M1038; M1039; M1040; M1041; M1042; M1043; M1044; M1045; M1046; M1047; M1048; M1049; M1050; M1051; M1052; M1053; M1054; M1055; M1056; M1057; M1058; M1059; M1060; M1061; M1062; M1063; M1064; M1065; M1066; M1067; M1068; M1069; M1070; M1071; M1072; M1073; M1074; M1075; M1076; M1077; M1078; M1079; M1080; M1081; M1082; M1083; M1084; M1085; M1086; M1087; M1088; M1089; M1090; M1091; M1092; M1093; M1094; M1095; M1096; M1097; M1098; M1099; M1100; M1101; M1102; M1103; M1104; M1105; M1106; M1107; M1108; M1109; M1110; M1111; M1112; M1113; M1114; M1115; M1116; M1117; M1118; M1119; M1120; M1121; M1122; M1123; M1124; M1125; M1126; M1127; M1128; M1129; M1130; M1131; M1132; M1133; M1134; M1135; M1136; M1137; M1138; M1139; M1140; M1141; M1142; M1143; M1144; M1145; M1146; M1147; M1148; M1149; M1150; M1151; M1152; M1153; M1154; M1155; M1156; M1157; M1158; M1159; M1160; M1161; M1162; M1163; M1164; M1165; M1166; M1167; M1168; M1169; M1170; M1171; M1172; M1173; M1174; M1175; M1176; M1177; M1178; M1179; M1180; M1181; M1182; M1183; M1184; M1185; M1186; M1187; M1188; M1189; M1190; M1191; M1192; M1193; M1194; M1195; M1196; M1197; M1198; M1199; M1200; M1201; M1202; M1203; M1204; M1205; M1206; M1207; M1208; M1209; M1210; M1211; M1212; M1213; M1214; M1215; M1216; M1217; M1218; M1219; M1220; M1221; M1222; M1223; M1224; M1225; M1226; M1227; M1228; M1229; M1230; M1231; M1232; M1233; M1234; M1235; M1236; M1237; M1238; M1239; M1240; M1241; M1242; M1243; M1244; M1245; M1246; M1247; M1248; M1249; M1250; M1251; M1252; M1253; M1254; M1255; M1256; M1257; M1258; M1259; M1260; M1261; M1262; M1263; M1264; M1265; M1266; M1267; M1268; M1269; M1270; M1271; M1272; M1273; M1274; M1275; M1276; M1277; M1278; M1279; M1280; M1281; M1282; M1283; M1284; M1285; M1286; M1287; M1288; M1289; M1290; M1291; M1292; M1293; M1294; M1295; M1296; M1297; M1298; M1299; M1300; M1301; M1302; M1303; M1304; M1305; M1306; M1307; M1308; M1309; M1310; M1311; M1312; M1313; M1314; M1315; M1316; M1317; M1318; M1319; M1320; M1321; M1322; M1323; M1324; M1325; M1326; M1327; M1328; M1329; M1330; M1331; M1332; M1333; M1334; M1335; M1336; M1337; M1338; M1339; M1340; M1341; M1342; M1343; M1344; M1345; M1346; M1347; M1348; M1349; M1350; M1351; M1352; M1353; M1354; M1355; M1356; M1357; M1358; M1359; M1360; M1361; M1362; M1363; M1364; M1365; M1366; M1367; M1368; M1369; M1370; M1371; M1372; M1373; M1374; M1375; M1376; M1377; M1378; M1379; M1380; M1381; M1382; M1383; M1384; M1385; M1386; M1387; M1388; M1389; M1390; M1391; M1392; M1393; M1394; M1395; M1396; M1397; M1398; M1399; M1400; M1401; M1402; M1403; M1404; M1405; M1406; M1407; M1408; M1409; M1410; M1411; M1412; M1413; M1414; M1415; M1416; M1417; M1418; M1419; M1420; M1421; M1422; M1423; M1424; M1425; M1426; M1427; M1428; M1429; M1430; M1431; M1432; M1433; M1434; M1435; M1436; M1437; M1438; M1439; M1440; M1441; M1442; M1443; M1444; M1445; M1446; M1447; M1448; M1449; M1450; M1451; M1452; M1453; M1454; M1455; M1456; M1457; M1458; M1459; M1460; M1461; M1462; M1463; M1464; M1465; M1466; M1467; M1468; M1469; M1470; M1471; M1472; M1473; M1474; M1475; M1476; M1477; M1478; M1479; M1480; M1481; M1482; M1483; M1484; M1485; M1486; M1487; M1488; M1489; M1490; M1491; M1492; M1493; M1494; M1495; M1496; M1497; M1498; M1499; M1500; M1501; M1502; M1503; M1504; M1505; M1506; M1507; M1508; M1509; M1510; M1511; M1512; M1513; M1514; M1515; M1516; M1517; M1518; M1519; M1520; M1521; M1522; M1523; M1524; M1525; M1526; M1527; M1528; M1529; M1530; M1531; M1532; M1533; M1534; M1535; M1536; M1537; M1538; M1539; M1540; M1541; M1542; M1543; M1544; M1545; M1546; M1547; M1548; M1549; M1550; M1551; M1552; M1553; M1554; M1555; M1556; M1557; M1558; M1559; M1560; M1561; M1562; M1563; M1564; M1565; M1566; M1567; M1568; M1569; M1570; M1571; M1572; M1573; M1574; M1575; M1576; M1577; M1578; M1579; M1580; M1581; M1582; M1583; M1584; M1585; M1586; M1587; M1588; M1589; M1590; M1591; M1592; M1593; M1594; M1595; M1596; M1597; M1598; M1599; M1600; M1601; M1602; M1603; M1604; M1605; M1606; M1607; M1608; M1609; M1610; M1611; M1612; M1613; M1614; M1615; M1616; M1617; M1618; M1619; M1620; M1621; M1622; M1623; M1624; M1625; M1626; M1627; M1628; M1629; M1630; M1631; M1632; M1633; M1634; M1635; M1636; M1637; M1638; M1639; M1640; M1641; M1642; M1643; M1644; M1645; M1646; M1647; M1648; M1649; M1650; M1651; M1652; M1653; M1654; M1655; M1656; M1657; M1658; M1659; M1660; M1661; M1662; M1663; M1664; M1665; M1666; M1667; M1668; M1669; M1670; M1671; M1672; M1673; M1674; M1675; M1676; M1677; M1678; M1679; M1680; M1681; M1682; M1683; M1684; M1685; M1686; M1687; M1688; M1689; M1690; M1691; M1692; M1693; M1694; M1695; M1696; M1697; M1698; M1699; M1700; M1701; M1702; M1703; M1704; M1705; M1706; M1707; M1708; M1709; M1710; M1711; M1712; M1713; M1714; M1715; M1716; M1717; M1718; M1719; M1720; M1721; M1722; M1723; M1724; M1725; M1726; M1727; M1728; M1729; M1730; M1731; M1732; M1733; M1734; M1735; M1736; M1737; M1738; M1739; M1740; M1741; M1742; M1743; M1744; M1745; M1746; M1747; M1748; M1749; M1750; M1751; M1752; M1753; M1754; M1755; M1756; M1757; M1758; M1759; M1760; M1761; M1762; M1763; M1764; M1765; M1766; M1767; M1768; M1769; M1770; M1771; M1772; M1773; M1774; M1775; M1776; M1777; M1778; M1779; M1780; M1781; M1782; M1783; M1784; M1785; M1786; M1787; M1788; M1789; M1790; M1791; M1792; M1793; M1794; M1795; M1796; M1797; M1798; M1799; M1800; M1801; M1802; M1803; M1804; M1805; M1806; M1807; M1808; M1809; M1810; M1811; M1812; M1813; M1814; M1815; M1816; M1817; M1818; M1819; M1820; M1821; M1822; M1823; M1824; M1825; M1826; M1827; M1828; M1829; M1830; M1831; M1832; M1833; M1834; M1835; M1836; M1837; M1838; M1839; M1840; M1841; M1842; M1843; M1844; M1845; M1846; M1847; M1848; M1849; M1850; M1851; M1852; M1853; M1854; M1855; M1856; M1857; M1858; M1859; M1860; M1861; M1862; M1863; M1864; M1865; M1866; M1867; M1868; M1869; M1870; M1871; M1872; M1873; M1874; M1875; M1876; M1877; M1878; M1879; M1880; M1881; M1882; M1883; M1884; M1885; M1886; M1887; M1888; M1889; M1890; M1891; M1892; M1893; M1894; M1895; M1896; M1897; M1898; M1899; M1900; M1901; M1902; M1903; M1904; M1905; M1906; M1907; M1908; M1909; M1910; M1911; M1912; M1913; M1914; M1915; M1916; M1917; M1918; M1919; M1920; M1921; M1922; M1923; M1924; M1925; M1926; M1927; M1928; M1929; M1930; M1931; M1932; M1933; M1934; M1935; M1936; M1937; M1938; M1939; M1940; M1941; M1942; M1943; M1944; M1945; M1946; M1947; M1948; M1949; M1950; M1951; M1952; M1953; M1954; M1955; M1956; M1957; M1958; M1959; M1960; M1961; M1962; M1963; M1964; M1965; M1966; M1967; M1968; M1969; M1970; M1971; M1972; M1973; M1974; M1975; M1976; M1977; M1978; M1979; M1980; M1981; M1982; M1983; M1984; M1985; M1986; M1987; M1988; M1989; M1990; M1991; M1992; M1993; M19

Tue Mar 27 09:32:17 2001

us-09-410-835-4.01ig.png

Page 127

CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
CC deterministic recombination therapy. V73508-V73566 represent PCR primers
CC for the detection of the *hprt* gene. V73567-V73570 represent PCR primers
CC The plasmids and probes are used experimentally for PCR, Southern
CC S1A/B/C and S2 and the K regions are used especially and M2 which is common
CC V73547-V73578).

50 Sequence 20 bp: 3 A: 5 C: 5 G: 7 T: 0 other:
Query Match 0.34; Score 20; DB 14; Length 20;
Matches 20; Conservative 0; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indexes 0; Caps

QY 628 gttataacgcgtgcgcgcgc 647
DB 1 gttataacgcgtgcgcgcgc 20

Tue Mar 27 09:32:17 2002

us-09-410-635-4.011g.png

Page 128

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.rmg

Page 131

Tue May 27 09:32:17 2001

us-09-410-035-4.011g.rdg

Page: 132

Tue Mar 27 09:32:17 2001

us-09-410-835-4.01ig.rng

Page 135

Tue Mar 27 09:32:17 2001

118-09-410-035-A 014

```

CC  malignancy, diseases of respiratory system, lung or thymus, digestive/endocrine
CC  disorders, infections and AIDS, viral infections, polypeptides are also useful for
CC  identifying their binding partners
XX
50  Sequence 610 BP: 187 A: 121 C: 103 G: 196 T: 3 other:

      Query Match
      Best Local Similarity 100.0%; Score 20; DB 20; Length 610;
      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
      Cy 383 ttaatgataaaataaaaaa 402
      |||
      Db 566 ttaatgataaaataaaaaa 585

RESULT 65
A26393
XX  A26393 standard; cDNA; 619 BP.
AC  A26393:
XX
XX  29-JUN-2000 (first entry)
DT
XX
XX  Human secreted protein gene 48 SPO ID:50.
DE
XX
XX  Human; secreted protein; diagnosis; cytotoxic; immunosuppressive;
XX  anti-infectious; immunology; neoplastic; neuroprotective; anti-leukic;
XX  antiproliferative; anti-infectious; anti-infectious; anti-infectious;
XX  antiproliferative; anti-infectious; gene therapy; cancer; inflammation;
XX  immune diseases; inflammation; blood disorder; tumor; ad-
XX
XX  Homo sapiens.
XX
XX  M0300006898-A1.
XX
XX  10-FEB-2000.
XX
XX  29-JUL-1999: 99ND-0521130.
XX
XX  10-JUL-1998: 98DS-0094657.
XX  06-AUG-1998: 98DS-0095456.
XX  06-AUG-1998: 98DS-0095456.
XX  12-AUG-1998: 98DS-0095455.
XX  12-AUG-1998: 98DS-0095319.
XX
XX  (HMM-) HMMAN GENE SCI INC.
XX
XX  Kozarski, J.G., Rosen C.A., Ruben S.M., Duan R., Moore P.N., Shi Y.;
XX  Lattier D., Wei Y., M.J., Florence K., Young P.E., Brewer L.A.;

```


Tue Mar 27 09:32:17 2001

US-09-410-835-4.011g.rdg

Page 163

Page 164

```

Query Match      0.39; Score 19: DB 19; Length 19:
Best Local Similarity 100.0%;
Matches 19: Consensitive 0; Mismatch: 0; Indels 0; Caps 0
QY 556 caacaccccaacacccgaag 574
      |||||
Db 1 caacaccccaacacccgaag 19

```

Tue Mar 27 09:32:17 2001

us-09-410-635-4.011g.rng

Page 164

DR P-1999-38506/32.
P-PSDB: Y36041.

XX New isolated human secreted proteins
XX
XX Claim 1: Page 364; 516pp; English.

CC This sequence represents an extended human secreted protein coding
CC sequence of the invention. The secreted proteins can be used in treating
CC or controlling a variety of human conditions. The secreted proteins may
CC or may act as tumor suppressors, growth factors, growth inhibitors, or
CC growth regulators, regulators of reproductive hormones or cell movement
CC or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
CC tumor inhibition activity. The DNA can be used in forensic procedures
CC individuals having genetic diseases. It may be used in the identification of
CC the gene corresponding to the extended cDNA. They are also useful for
CC also be used for gene therapy to control or treat genetic diseases.

50 Sequence 625 BP: 138 A; 181 C; 114 G; 168 T; 4 other:

Query Match 0.31; Score 19; DB 20; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 383 tatgtaaaaaaaaaaaaa 401
607 tatgtaaaaaaaaaaaaa 625

RESULT 87
ID 532996 standard: cDNA; 760 BP.

XX 532996:
XX 14-MAR-2000 (first entry)

DE Human prostate tumor cDNA library derived EST fragment #139.

XX Pancreatic tumor: EST: expressed sequence tag; human; cytosolic;

XX treatment: db.

XX Homo sapiens.

XX D01982030-A1.

XX 04-NOV-1999.

Tue Mar 27 09:32:17 2001

us-09-410-835-4.o11g.rng

Page 171

XX Mm up.

XX M09955728-A2.

XX 04-NOV-1999.

XX 27-APR-1999; 99NO-CA00375.

XX 27-APR-1998; 98CA-220201.

XX 05-FEB-1999; 99DS-01187319.

XX (HSCR-) HSC RES 6 DEY LP.

XX Egan SE, Wang M, Sengar A;

XX WPI: 2000-053802/04.

XX New nucleic acid encoding Eas1 and 2 proteins. Involved in regulation
XX of endocytosis, used e.g. for treating cancer or preventing viral
XX infection

XX Discloure: Page 55-56; 99pp; English.

CC The present invention specifically describes mammalian Eas1 and 2
CC proteins and their splice variants (Eas1-E1 and Eas1-E2) and Eas1-E2
CC mediated endocytosis (as a complex with Eas1 protein). Eas1-E2
CC trafficking and actin cytoskeleton. Generally (1) (or its (ant)agonists,
CC fragments and inactive mutants); (2) specific antibodies (Ab);
CC expression of Eas1 genes or anti-polymerase; agents that downregulate
CC used to treat diseases associated with undesirable endocytosis and
CC resulting changes in cellular function. Particularly expression of
CC Eas1-E2 is used to block clathrin-mediated endocytosis in vivo or in cell
CC selected cells. (ant)agonists of (1) or (2) are used to promote
CC proliferation of cells that can be stimulated to proliferate by a growth
CC factor receptor and similar compounds (also inactive Eas1 mutants) can be
CC used to prevent viral infection. Endocytosis may also be regulated, in
CC vivo or in cell culture, by (ant)agonists of (1) or (2) or by Eas1-E2
CC dynamic to the complex. Generally conditions that can be used to bind
CC cancer; abnormal cell division or migration; viral infection; or abnormal
CC protein sequence represents a mouse cDNA clone Eas1-E2 interacting clone.

Query Match 0.31; Score 19; DB 21; Length 801;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Tue Mar 27 09:32:17 2001

us-09-410-835-4.o11g.rng

Page 170

XX 28-APR-1998; 98DE-1020190.

XX 28-APR-1998; 98DE-1020190.

XX (MENA-) METACIN GES GENOFORCHUNG BKH.

XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

XX WPI: 1999-62136/54.

XX P-PSDB: Y74233; Y74234; Y74235; Y74236; Y74237.

XX New human nucleic acid sequences from pancreatic tumors, and related
XX proteins

XX Claim 2: Page 293; 502pp; German.

CC This invention describes novel polypeptides and their encoding nucleic
CC acids. The polypeptides and nucleic acids have cytosolic
CC activity. The sequences are also useful in producing transgenic
CC compositions for treatment of pancreatic tumors. 253858-253914 represent
CC expressed sequence tag (EST) fragments derived from a human pancreatic
CC cDNA library and which encode the proteins represented in
CC Y73814-Y74232.

50 Sequence 760 BP: 250 A; 126 C; 136 G; 248 T; 0 other:

Query Match 0.31; Score 19; DB 20; Length 760;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 384 tatgtaaaaaaaaaaaaa 402
737 tatgtaaaaaaaaaaaaa 755

RESULT 88
ID 239022 standard: cDNA; 801 BP.

XX 239022:
XX 239022:

XX 28-FEB-2000 (first entry)

XX House novel cDNA clone 18/25 3'-end Eas1-E2 interacting clone.

XX Mouse; murine; Eas1; Eas2; endocytosis; vesicular trafficking;

XX regulation; actin cytoskeleton; detection; cancer; infection;

XX E1-domain and SH3-domain regulator of endocytosis; anticancer;

XX antiproliferative; antiviral; ss.

Tue Mar 27 09:32:17 2001

us-09-410-835-4.o11g.rng

Page 172

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 384 tatgtaaaaaaaaaaaaa 402
737 tatgtaaaaaaaaaaaaa 755

RESULT 89
ID 239022 standard: cDNA; 801 BP.

XX 239022:
XX 239022:

XX 26-JUN-1998 (first entry)

XX H. pylori ORF 05ac2020orf58.

XX Cytoplasmic; vacuole; prevention; treatment; infection; envelope;

XX identification; binding compound; bacteria; life cycle; activator;

XX Helicobacter pylori.

XX Helicobacter pylori.

XX Key

XX Location/Qualifiers

XX 1-879

XX /note="no stop codon given"

XX M09737044-A1.

XX 09-OCT-1997; 97NO-0605223.

XX 27-MAR-1997; 97NO-0605223.

XX 06-DEC-1996; 96DS-0761318.

XX 29-MAR-1996; 96DS-0628811.

XX 25-OCT-1996; 96DS-0761318.

XX 28-OCT-1996; 96DS-0761318.

XX (ASTR-) ASTRA AB.

XX Ale RA, Smith D;

XX WPI: 1997-503122/46.

XX P-PSDB: M5524.

XX Helicobacter pylori nucleic acid sequences and encoded

XX polypeptide(s) - useful in vaccines to treat or prevent H. pylori

XX infection and for diagnosis of H. pylori infection

Tue Mar 27 09:32:17 2001

US-09-410-835-4.01ig.rmq

Page 179

Tue Mar 27 09:32:17 2001

us-09-410-B35-4.011g.rmg

Page 180

Page 180

KM Neural: reproductive; immune disorder; immunodeficiency; infection;
 KM Lymphoma; demyelinating disease; autoimmunity; cancer; inflammation;
 KM Anemia; haemorrhage; Alzheimer's disease; Parkinson's disease;
 KM Huntington's disease; Tourette syndrome; multiple sclerosis; meningitis;
 KM Alzheimer's disease; obsessive compulsive disorder;
 KM viral prophylaxis; degenerative disease; infectious disease;
 KM cardiovascular disorder; food additive; preservative; chromosome 11; ds.
 XX Homo sapiens.
 XX
 XX W020011014-AL.
 PD 02-MAR-2000.
 XX 24-AUG-1999: 99NO-0513310.
 XX 25-AUG-1998: 98US-0097917.
 PR 31-AUG-1998: 98US-0098634.
 XX (HUM-1) HUMAN GENE: CCL1 INC.
 PI Moore PA, Ruben SH, Olsen HS, Shi Y, Rosen CA, Florence MA,
 PI Soppet DR, Lafleur DW, Endress CA, Emmer R, Komatsu G,
 PI Duan RD.
 DR WPI: 2000-224656/19.
 DR P-PSDB: Y91375.
 XX
 XX Novel secreted protein and corresponding DNA molecules that can be
 XX used to prevent, treat and diagnose disease in humans, for example,
 XX Alzheimer's, cancer, and immune disorders.
 PS
 PS Claim 1: Page 332-333: 416pp: English.
 CC The polynucleotide sequences given in A26381 to A26386 encode the human
 CC secreted proteins given in Y9134 to Y9149.
 CC Examples of the activities are: neuroprotective; neurotrophic; neurogenic;
 CC entimatic; cerebroprotective; immunomodulatory; anti-microbial; cardiac;
 CC vasotropic; neuroprotective; immunomodulatory; anti-microbial; cardiac;
 CC treat or ameliorate a medical condition, e.g. by protein or gene therapy.
 CC Conditions treatable by the proteins of the invention include neural,
 CC infection, or immune disorders, especially immunodeficiency,
 CC general microbial infection, inflammation, aneurysm, and cancer,
 CC specific examples include: Alzheimer's disease, Parkinson's,
 CC Huntington's, Tourette syndrome, multiple sclerosis, meningitis;
 CC disorder and viral prophylaxis; anemia; dementia; obsessive compulsive
 CC disorder and viral prophylaxis; degenerative disease; infectious disease;
 CC be used in the detection of disorders associated with the function of the

Tue Mar 27 09:32:17 2001

us-09-410-835-4-olig.rng

Page 187

DR P-PSDB: W79093.
 PT New polynucleotide(s) encoding secreted human proteins derived
 PT from human foetal kidney, adult testes and adult or foetal brain
 PT CDNA libraries
 XX
 XX Claim 27: Page 80-83: 112pp: English.
 CC This full-length cDNA clone, designated dn904_2, codes for a novel
 CC secreted human protein (see W79093). It was isolated from a human
 CC foetal brain cDNA library using methods which are selective for
 CC CDNA clones encoding secreted proteins or proteins identified as encoding
 CC a secreted or transmembrane protein on the basis of the nucleotide
 CC analysis of the encoding protein. The nucleotide sequence shows
 CC homology to some database sequences, and may contain an Alu
 CC insertion element. The invention provides cDNA clones (see
 CC W6477-87) from human foetal kidney, adult testes and adult or
 CC foetal brain cDNA libraries that code for secreted proteins (see
 CC W79087-97). These clones are deposited as ATCC 98364. The
 CC polynucleotides and proteins are predicted to have useful
 CC preventing or ameliorating effects on a wide range of diseases and
 CC anomalies, although no supporting data is given. Suggested
 CC activities include nutritional, immune stimulating (e.g. as
 CC activator/inhibitor of growth, hematopoiesis, regulating, tissue growth,
 CC thymolytic, receptor/ligand, anti-inflammatory, coadjuvant/tumour
 CC invasion suppressor and tumour inhibition activities. The
 CC polynucleotides are also stated to be useful for gene therapy.
 SO Sequence 2547 BP: 640 A: 476 C: 416 G: 1012 T: 3 other:
 XX
 XX Query Match 0.31: Score 19: DB 19: Length 2547;
 XX Best Local Similarity 100.0%: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 XX Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 XX
 XX 3020 AAAAAAAAAAATGCGA 3018
 XX 333 ATCTTCAAAATCAATCCCA 315
 XX
 XX RESULT 99
 XX T58898/c
 XX ID T58898 standard: cDNA: 2883 BP.
 XX XX T58898:
 XX 28-APR-1997 (first entry)
 XX
 XX C-Delta-1 gene (alternatively spliced variant).

Tue Mar 27 09:32:17 2001

us-09-410-835-4-olig.rng

Page 186

CC protein, for example, the detection of developmental disorders,
 CC sexually-linked disorders, or disorders of the cardiovascular system,
 CC T58898/c
 CC ID T58898 standard: cDNA: 2547 BP.
 XX 384 TATGTAATGAAAAAAAAA 402
 XX 2396 TATGTAATGAAAAAAAAA 2414
 XX
 XX RESULT 98
 XX T58898/c
 XX ID T58898 standard: cDNA: 2547 BP.
 XX 384 TATGTAATGAAAAAAAAA 402
 XX 2396 TATGTAATGAAAAAAAAA 2414
 XX
 XX DT 11-JAN-1999 (first entry)
 XX
 XX Human secreted protein dn904_2 cDNA.
 XX Secreted protein: human: dn904_2: ds.
 XX Homo sapiens.
 OS
 OS Key Location/Qualifiers
 PS 1563: 1568
 PS CDS /'tag' 4
 XX W09841539-A2.
 PD 24-SEP-1998.
 XX 19-MAR-1998: 98NO-0505474.
 XX 18-MAR-1998: 98US-0040963.
 PR 19-MAR-1997: 97US-0820493.
 XX (GCHN) GENETICS INST INC.
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Metberg D,
 PI Racie LA, Spaulding V, Tracy M.
 DR WPI: 1998-52163/44.

Tue Mar 27 09:32:17 2001

us-09-410-835-4-olig.rng

Page 188

XX C-Delta-1: cell proliferation; nervous system disorder;
 XX tissue regeneration; notch; cervix cancer; breast cancer;
 XX lung cancer; colon cancer; melanoma; seminoma;
 XX neurogenesis; therapy; ss.
 OS
 OS Gallus sp.
 PS
 PS Key Location/Qualifiers
 PS 2: 2499
 PS CDS /'tag' 4
 XX W09701571-A1.
 PD 16-JAN-1997.
 XX 28-JUN-1995: 96NO-0511178.
 XX 28-JUN-1995: 96NO-0511178.
 XX 28-JUN-1995: 96NO-0511178.
 XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 PA (UYTA) UNIV YALE.
 XX Altavilla-Traasnas S, Gray GE, Henrique D, Ish-Horowicz D,
 XX Lewis J.
 DR WPI: 1997-100159/03.
 DR P-PSDB: W00876.
 PT New vertebrate Delta protein, DNA and antibodies - for treating and
 PT preventing cancer, nervous system disorders and for tissue
 PT regeneration
 XX
 XX Disclosure: Fig 1B1-1B2: 135pp: English.
 CC The C-delta-1 gene (T58898) codes for the chick homologue (W00876)
 CC of Drosophila Delta, a protein that binds to Notch protein. It was
 CC isolated from a cDNA library from stage 4-6 embryos using
 CC primers (see also T59455-56) based on the Delta cDNA sequence.
 CC shorter variant (T58897) was also identified. C-delta-1 expression
 CC appears to be the earliest known marker for prospective neurons.
 CC Also been isolated human (T59400, T59464) Delta-1 sequences have
 CC been identified in chick (T58898) and human (T59400, T59464) Delta-1
 CC Delta polypeptides and (including antisense sequence) protein of in
 CC the treatment of disorders of cell fate or differentiation, such as
 CC cancer, and nervous system disorders, or to promote tissue
 CC regeneration and repair.
 SO Sequence 2883 BP: 638 A: 850 C: 792 G: 593 T: 2 other:

Query Match	0.31	Score 19:	DB 18:	Length 2883:
Best Local Similarity	100.0%	Pred. No. 1e+02:		
Matches 19:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0
07	3220	gtttatattatgagatgacg	3218	
Db	2818	CTTATATATTAACAAACACG	2800	
RESULT 100				
ID	T16857	standard: cDNA, 4089 bp.		
AC	T16857.			
XX				
D7	20-MAY-1996	(first entry)		
XX				
D8		bovine endothelial nitric oxide synthase cDNA clone pBOS13.		
XX				
KM	nitric oxide synthase; NOS: endothelial cell; diagnosis;			
KM	gene therapy; aa.			
XX				
OS	Bos taurus.			
PH	Key	Location/Qualifiers		
PH	CD5	/50..3647		
PT		/terminal_except pos:2187..2189; aa:A1a		
PT		/trnal_except_pos:2190..2192; aa:K7g		
XX				
XX	US5458539-A.			
XX				
PD	13-MAR-1996.			
XX				
XX				
XX	02-JUL-1992:	9205-0908245.		
PR	02-JUL-1992:	9205-0908245.		
XX				
XX	(DACC) DALTECH PHARM CO LTD.			
PI	Alexander RM, Harrison DC, Murphy JZ, Michals K;			
PI	WPI: 1996-159689/16.			
XX	P-7558b; R39350.			
XX				
XX	DNA encoding bovine endothelial nitric oxide synthase - used as			
PT	probe for research and diagnostic purposes, and therapeutically to			
XX	increase nitric oxide prodn. in blood vessels			
XX	Claim 2: Column 15-20: 21pp: English.			

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.rng

Page 191

```

DR      P-PSDB: Y17500.
XX
XX      New invertase precursor - cloned from Schizosaccharomyces pombe
XX      Ps
XX      Clain 1; Page 6-9; 15pp; Japanese.
XX
XX      The present sequence encodes an invertase precursor (I) of a mitotic
XX      yeast, Schizosaccharomyces pombe, designated inv1. The molecular entity
XX      of the yeast, Schizosaccharomyces pombe was
XX      clarified
XX
XX      Sequence 4748 BP: 1474 A; 908 C; 820 G; 1546 T; 0 other;
XX
XX      Query Match
XX      Best Local Similarity 0.3%; Score 19; DB 20; Length 4748;
XX      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      Qy 1060 atccgacgacgcacgaagc 1078
XX      Db 501 atccgacgacgcacgaagc 483
XX      |||||||||||||||||||
XX
XX      RESULT 107
XX      X57323/5
XX      X57323 standard; DNM; 4748 BP.
XX      AC X57223;
XX
XX      26-JUN-1999 (first entry)
XX      DE
XX      S. pombe invertase DNA.
XX
XX      Inducible promoter; Invertase; catabolic Inhibition; vector;
XX      extracellular expression; foreign gene; regulation expression; ss.
XX      OS Schizosaccharomyces pombe.
XX      M099323233-A1.
XX      PD
XX      14-MAY-1999.
XX
XX      30-OCT-1998; 98MO-JP04929.
XX      PR
XX      31-OCT-1997; 97JP-0334608.
XX      (ASNC ) ASANI GLASS CO LTD.
XX      PI
XX      Hama T, Kuwagaki H, Tonda H;
XX      WPI: 1999-313344/26.
XX

```

```

CC A cDNA clone (716857), designated pBOS13, codes for bovine
CC endothelial nitric oxide synthase (NOS) (R93930). pBOS13 was
CC generated by RT-PCR from total RNA isolated from bovine aortic endothelial
CC cells by screening with a cDNA library prepared from bovine aortic endothelial
CC gene can be used in the presn. of probes (see 71686-60). or may be
CC transcribed into host cells for prodn. of large vols. of endothelial
CC cDNA.
CC NOS. Alternatively, the gene is transcribed into blood vessels in
CC vivo to give a threefold increase in nitric oxide prodn.
XX
XX Sequence 4088 BP; 761 A; 1400 C; 1237 G; 691 T; 0 other:
XX
XX Query Match 0.3% Score 19. DN 17. Length 4089.
XX Best Local Similarity 100.0% Pwd No. 97
XX Matches 19. Conservative 0. Mismatches 0. Indels 0. Gaps 0
XX
XX 04 taatgataaaataaaataaa 402
XX |||||
XX 4071 taatgataaaataaaataaa 4089
XX
XX RESULT 101
XX X76320/C
XX ID X76320 standard: DNA: 4748 BP.
XX XX
XX XX X76320:
XX
XX 05-AUG-1999 (first entry)
XX
XX Schistosomacanthomyes pombe Invertase precursor inv1+ encoding DNA.
XX XX
XX Schistosomacanthomyes pombe: invertase precursor: mitotic yeast: inv1+;
XX molecular entity: ds.
XX
XX Schistosomacanthomyes pombe.
XX
XX Location/Qualifiers
XX CD5 2810..4555
XX /tag = a
XX
XX JP11127865-A.
XX
XX 18-MAY-1999.
XX
XX 31-OCT-1997: 97JP-0316607.
XX
XX 31-OCT-1997: 97JP-0316607.
XX (NASG) ASMNI GLASS CO LTD.
XX
XX #PI: 1999-150326/30.
XX

```

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.png

Page 192

```

DR      P-P508.  Y08199.
XX      Promoter and secretory signal sequences from inverteate gene of
PT      Schistosomacromyces pombe
PS      Claim.2: Page 48-52: 67pp: Japanese.
XX      CC
CC      This invention describes a novel promoter region of the moiety relating
CC      to the inverteate gene of Schistosomacromyces
CC      pombe. The products of the invention are the identification of
CC      a vector which allows extracellular expression of a foreign gene,
CC      regulated by the presence or absence of a specific nutrient such as
CC      glucose and resalate in the easy regulated expression of foreign genes
CC      in a yeast system.
XX      CC
XX      50      Sequence 4748 BP: 1474 A; 908 C; 820 G; 146 T; 0 other:
               Query Match          0.3%; Score 19; Db 20; Length 4748;
               Best Local Similarity 100.0%; Pred. No. 96;
               Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
               Oy 1060 accgaagacaggaatcaaaagc 1078
               |||||
               Db 501 ATCCGACGATCAAAAGT 483
RESULT 103
X2454/c
X2454/c standard; DNA: 5790 BP.
AC AC X2454:
XX      07-JUN-1999 (first entry)
PT      Bovine myostatin genomic DNA
DE
DE      Myostatin; cattle; bovine; transforming growth factor beta;
XX      double muscling; muscle hypertrophy; transgenic animal; ns.
XX      CC
XX      05      Bos taurus.
XX      CC
XX      Key Location/Qualifiers
XX      CDS             1..418
XX      /tag          /tag a
XX      /note         "contains introns"
XX      exon           454..826
XX      /number       1
XX      /intron        827..2652
XX      /tag          /tag c
XX      Intron

```

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.rng

Page 195

Tue Mar 27 09:32:17 2001

us-09-410-835-4.0119.rng

Page 196

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.png

Page 203

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.rmg

Page 204

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.rmg

Page 204

FT	promoter	/tag= bq	2426..24315
FT	exon	/complement(24600..24649)	
FT	exon	/tag= ba	30550..31665
FT	exon	/tag= ba	30550..30863
FT	polyA_site	/tag= bu	32483..32488
FT	repeat_region	/tag= bu	32483..32488
FT	repeat_region	/tag= bv	31659..33870
FT	exon	/note= "AU repeat family"	
FT	exon	/complement(33787..33867)	
FT	repeat_region	/tag= by	complement(24638..34966)
FT	exon	/note= "TTCGSR2 repeat family"	
FT	exon	/complement(34879..34941)	
FT	exon	/tag= Dz	
Query Match		0.3% Score 15; DB 20; Length 68940;	
Blast Local Similarity	100.0%; Pred. No. 78;		
Matches 19; Mismatches 0; Indels 0; Gaps 0			
Yr 389	aaaaaaaaaaaatgcctc 407		
Dz 64556	aaaaaaaaaaaaaaagtcct 64574		
RESULT 114			
ID 10	286967 standard: DNA; 162450 BP.		
AC 286967:			
XN 16-MAY-2000	(first entry)		
DE Retinoblastoma binding protein-7 genomic DNA sequence.			
KX RRP-7, retinoblastoma binding protein-7, abnormal cell proliferation,			
KM diagnosis: retinoblastoma; thyroid dysplasia; prostatic;			
Lymphoma; ds.			
FN lymphatic hypertrophy; cancer; sarcoma; neoplasm; leukemoid;			
OX Homo sapiens.			
CX			
NN MO200000607-A1.			
CX			

Tue May 27 09:32:17 2001

us-09-410-835-4.011g.rng

Page 215

AC V75359; Z

XZ 22-MAR-2000 (first entry)

DE H. pylori cag A primer cagM1.

XX PCR primer; probe: vacA; cagA; detection: vacuolating toxin; VDO;

XX Intectively determinat gene; cytotoxin associated gene; ulcer-specific;

KU Intectively determinat gene; cytotoxin associated gene; ulcer-specific;

KK adenocarcinoma; mucosa-associated lymphoid tissue MALT; B-cell;

CC S region; StA; StB; StC; StD; M region; M1; M2; ss.

OK Helicobacter pylori.

PX h09816658-A2.

PN 23-MAR-1998.

XX 10-OCT-1997; 97MO-EPOS614.

PP 16-OCT-1996; 96EP-0870131.

PR 09-SEP-1997; 97EP-0070133.

PA (INDO-) DDL BIOGENETICS NV.

XX (DDND-) DDL BV.

PI Quinte W, Van Doorn L.

DR WP1: 1598 -233300/72.

XX Method for detecting and/or typing Helicobacter pylori strains -

P7 compiles use of primers and probes based on vacA and cagA gene

XX claim 2: Page 44: 122pp: English

CC This invention describes a novel method for the detection and/or typing

CC of Helicobacter pylori strains present in a sample using PCR primers and

CC probes to detect regions of the vacuolating toxin (vacA) gene and other

CC genes. The method involves amplifying DNA from a sample containing a

CC strain according to the VDO alleles present in that population of a

CC strain. The resulting determinant genes are the genetic elements involved

CC in determining, determining, and marking the infectivity and/or

CC detecting H. pylori strains in a sample. The method provides a way of

CC detecting H. pylori strains in a sample which can provide a representative

CC of chronic active gastritis, gastric and duodenal ulcers, gastric

CC adenocarcinomas, mucosa-associated lymphoid tissue (MALT), and/or

CC cancer. The method also provides a way of detecting H. pylori strains

CC and probes used in the detection of H. pylori strains in a sample. The

CC primers and probes are used especially to detect the vacA genes

CC StA/B/C and StD and the M regions M1 and M2 which are represented in

PB	06-JAN-2000.
PD	30-JUN-1999:
PR	99NOV-1801342.
PP	30-JUN-1998:
PR	98UUS-0093115.
PR	10-DEC-1998:
PR	98OUS-0111909.
XX	(GZER) GENSET.
P1	Bougaerret L;
P2	wpi. 2000-11170/10.
XX	
XX	Newel nucleic acid and polymorphic markers used for diagnosis of
PT	disease, especially those involving abnormal cell proliferation and
PT	differentiation.
PT	
PT	claim 1: Page 118-163; 22zip; English.
XX	
XX	This sequence represents the retinoblastoma binding protein-7 (RBP-7)
CC	nucleic acid sequence of the invention. The RBP-7 coding sequence and
CC	equivalent sequences are useful for identifying the overproduction of the
CC	protein and for expressing heterologous nucleic acid/protein production or
CC	derived from the RBP-7 nucleotide and detection methods. RBP-7 biologic
CC	useful for DNA amplification and detection methods. RBP-7 biologic
CC	to alterations in 3'-2870039 are useful for diagnosis of disease related
CC	to alterations in 3'-2870039 are useful for diagnosis of disease related
CC	gene and for prognosis/diagnosis of an eventual treatment with the RBP-7
CC	therapeutic agents, especially agents acting on pathologies involving
CC	abnormal cell proliferation and/or differentiation, these include
CC	neuroblastoma, neuroblastoma, neuroblastoma, neuroblastoma, cancer,
CC	including breast cancer, sarcoma and other neoplasms, lymphoma, and
CC	colon cancer, lung cancer, prostate cancer, various leukemias, and
CC	lymphomas. RBP-7 antibodies are useful as diagnostic agents.
SQ	Sequence 162450 BP: 54565 A: 30661 C: 32637 G: 53673 T: 14 others;
Query Match	0.3%
Best Local Similarity	100.0%
Matches 19: Conservative	0: Mismatches
Indels	0: Caps
Gaps	0
Cy	2642 attcacaacatggccaaca 2650
Dn	132868 ATTCAAAATTCAGTAAA 132850
Resung 115	
V73595.C	
ID	V73595 standard: Dm. 18 BP.

Tue Mar 27 09:32:17 2001

us-09-410-835-4.01ig.rnq

Page 216

1	RESULT 121
2	251317/c
3	AC 531197
4	AC 531197
5	06-JUN-2000 (first entry)
6	Primer R66.0, for cDNA synthesis of Ischemic heart mRNA.
7	Ischemia; heart disease; human; Pop980; cardiomyopathy; cardiac;
8	modulator; treat; prevention; diagnosis; primer: 58.
9	Synthetic.
10	Homoe sapiens.
11	NC020010.142: AL
12	XX 09-MAR-2000.
13	PD 01-SEP-1999: 5980-US20015.
14	PZ 01-SEP-1999: 9805-009683.
15	PR (GENE): GENE LOGIC INC.
16	XX Elmhurst IL
17	WIPI: 2000-237720/20
18	Isolated nucleic acids encoding a proteins that is differentially
19	expressed during ischemic heart disease and ischemic cardiomyopathy,
20	useful for preventing, diagnosing and treating cardiac disease .
21	Example 1: Page 56: 61pp: Emulstat.
22	The present sequence is the primer, R66.0, used for cDN synthesis of the
23	differentiall isolated, assayed, sequenced, and cloned, cDNA that
24	consists of the base anchored oligo (dt) primer and is used with other
25	components of the first-strand cDN synthesis. The protein Pop980, as
26	expressed in heart, brain, lung, placenta, skeletal muscle, kidney and
27	other tissues, is a protein that is differentially expressed in heart
28	defect and quantify homologous sequences in samples. Pop980, protein can
29	be used to identify modulators, that can be used for treatment, diagnosis
30	and prevention of diseases associated with inappropriate expression and
31	cardiomyopathy.
32	Sequence 40 BP: 7 A: 8 C: 4 G: 21 T: 0 other:


```

PS      Example 1: Page 137: 500bp: English.
XX
CC      The Engrailed Sequence Tag was isolated from a human brain cDNA
CC      library as part of a larger set of ESTs available from the
CC      library for human genes transcribed in vivo. They can be used to facilitate
CC      tagging of most human genes, for mapping locations of expressed genes
CC      (e.g. in situ hybridization), or for genetic identification, for mapping
CC      locations of disease-associated genes, or for genetic identification, for
CC      mapping locations of disease-associated genes, or for genetic identification,
CC      type, and for PCR of alternative sequences, probes and constructs.
CC      ENF00365 has a "poor" coding probability as evaluated using the
CC      see also G99041, G99042, G99043, G99044, G99045, G99046, G99047, G99048,
XX
XX      Sequence 355 BP: 87 A; 99 C; 61 G; 107 T; 1 other:
XX
XX      Query Match
XX      Best Local Similarity: 0.3%; Score 18; DB 14; Length 355;
XX      Matches: 18; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0.
XX
XX      3173 ataccacataataacatg 3190
XX      |||||||
XX      302 ataccacataataacatg 319
XX
XX      RESULT 136
XX      ID: 0035
XX      ID: 010253 standard; DN: 360 BP.
XX      Q10253:
XX
XX      27-MAR-1991 (first entry)
XX
XX      Synthetic version of Alcohol Dehydrogenase 2 promoter.
XX      urate oxidase; uricase; human growth hormone; ADH2, ds.
XX
XX      EP040461-A.
XX
XX      16-JAN-1991.
XX
XX      13-JUL-1990: 90EP-040203.
XX
XX      06-FEB-1990: 90EP-000138.
XX      29-OCT-1989: 89EP-000350.
XX      09-DEC-1989: 09EP-001746.
XX
XX      (SNP) 5AN0P1 SA.

```


PD 09-OCT-1997.
 PF 01-APR-1997: 97MO-0505306.
 PR 22-AUG-1996: 9605-0035788.
 PR 02-APR-1996: 9605-0014690.
 PA (SMK) SMITHLINE BECCAM CORP.
 PA (SMK) SMITHLINE BECCAM P.L.C.
 PI Black HT, Hodgson JE, Knowles D.C., Nicholas RO.
 PI Stodola RK.
 PI WPI: 1997-50311/46.
 DR P-PSDB: Y13137.
 XX Nucleic acids encoding pneumococcal polypeptide(s) - useful in
 XX vaccines, drug screening, etc
 PS Claim 5: Page 160: 35pp: English.
 CC X10724 to X10946 represent genomic DNA sequences isolated from
 CC streptococcus pneumoniae strain 0100931. These genomic DNA sequences
 CC isolated from streptococcus pneumoniae can be used, in the proteins, insert
 CC streptococcal infections and in assays for identifying compounds that
 CC inhibit or activate the activity of the proteins. The antagonists can
 CC protect an individual having need to inhibit a bacterial
 CC protein secreted by streptococcus pneumoniae can be used to induce a
 CC protective immune response in mammals.
 SQ Sequence 425 BP: 154 A: 81 C: 86 G: 104 T: 0 other:
 Query Match 0.38: Score 18: DB 18: Length 425.
 Best Local Similarity 100.0%: Pred. No. 3: 1e+02:
 Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 4744 tttcttcttcttcttcttctt 4761
 DB 90 tttcttcttcttcttcttctt 73
 RESULT 140
 XN 10-APR-1998: 98MO-0506954.
 XN X97675 standard: DNM: 471 BP.
 XN X97675:
 XN 13-SEP-1999 (first entry)
 XX

Tue Mar 27 09:32:17 2001

us-09-410-835-4.019.rng

Page 247

Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 385 aatgaataaataaataaataa 402
 DB 454 aatgaataaataaataaataa 471
 RESULT 141
 XN 10-APR-1998: 98MO-0506954.
 XN X97675 standard: DNM: 491 BP.
 XN X97675:
 XN 13-SEP-1999 (first entry)
 XX

27-APR-1999 (first entry)
 DE EST clone AJ143.
 XX
 XX Represented sequence tag: secreted protein, hematopoietic regulator;
 XX 10-APR-1997: 9705-0835913.
 XX Chemotaxis; chemokinesis; hematopoietic; tumor suppressor; EST; human;
 XX receptor; ligand: anti-inflammatory; tumor inhibitor; de.
 XX Homo sapiens.
 XX MO9845435-A2.
 XX 15-OCT-1998.
 XX 10-APR-1998: 98MO-0506954.
 XX 10-APR-1997: 9705-0835913.
 XX (GEM) GENETICS INST INC.
 XX Agostino M, Jacobs K, Lavallie ER, McCoy JM, Weisberg D;
 XX Rele LA, Spaulding V, Treacy W.
 XX WPI: 1999-070076/06.
 XX
 XX New polynucleotides encoding human secreted proteins - derived from
 XX cDNA, human blood, kidney, foetal lung, placenta, testes, brain,
 XX ovary, placenta, testis and colon cDNA libraries
 PS Claim 1: Page 182: 63pp: English.
 XX
 XX This sequence represents an expressed sequence tag (EST), and is a
 XX partial sequence of a human secreted protein. The protein is
 XX all secreted EST sequences isolated from various human
 XX sources. The EST sequences and proteins encoded by them are predicted to
 XX have useful biological activities which would make them suitable for
 XX treating, preventing or ameliorating medical conditions in humans and

Tue Mar 27 09:32:17 2001

us-09-410-835-4.019.rng

Page 246

DE Extended human secreted protein coding sequence, SEQ ID NO: 139.
 KW Secreted protein, human: cytokine; cellular proliferation; cell movement;
 KW cellular differentiation; immune system regulator; anti-inflammation;
 KW hematopoietic regulator; tissue growth regulator; tumor inhibitor;
 KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
 KW genetic disease; as.
 XX Homo sapiens.
 XX MO991326-A2.
 XX 24-JUN-1999.
 XX
 XX 17-DEC-1998: 98MO-1802122.
 XX 10-AUG-1998: 98MO-0086116.
 XX 17-DEC-1997: 9705-0066957.
 XX 09-FEB-1998: 9805-0074121.
 XX 13-APR-1998: 9805-0081563.
 XX (GEM) GENETICS INST INC.
 XX Bouguetier L, Duclert A, Dumas Milne Edwards J;
 XX WPI: 1999-085906/32.
 XX P-PSDB: Y15991.
 XX New isolated human secreted proteins
 PS Claim 1: Page 267-268: 51pp: English.
 XX
 XX This sequence represents an extended human secreted protein coding
 XX sequence of the invention. The secreted proteins can be used in treating
 XX or controlling a variety of human conditions. The secreted proteins may
 XX be used in the treatment of human conditions such as: cellular proliferation
 XX or may act as immune system regulators, hematopoietic regulators, tissue
 XX growth regulators, regulators of reproductive hormones or cell movement
 XX or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
 XX or immunomodulatory activity. The DNA can be used in forensic procedures
 XX to identify individuals having genetic diseases resulting from abnormal
 XX individuals having genetic diseases resulting from abnormal expression of
 XX the genes corresponding to the extended cDNAs. They are also useful for
 XX constructing a high resolution map of the human chromosomes. They can
 XX also be used for gene therapy to control or treat genetic diseases.
 SQ Sequence 471 BP: 105 A: 120 C: 120 G: 126 T: 0 other:
 Query Match 0.38: Score 18: DB 20: Length 471.
 Best Local Similarity 100.0%: Pred. No. 3e+02:
 Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 3961 ggtttcaaaatttttttttt 3978
 DB 250 GCTTCCAAAATTCTTA 233
 RESULT 142
 XN 10-APR-1998: 98MO-0506954.
 XN X97675 standard: DNM: 507 BP.
 XN X97675:
 XN 13-SEP-1999 (first entry)
 XX

Tue Mar 27 09:32:17 2001

us-09-410-835-4.019.rng

Page 248

XX animals, although no supporting data is given. Suggested activities
 XX include nutritional activity, immune stimulating or suppressing activity,
 XX hematopoietic activity, hematopoietic activity, hematopoietic
 XX activity/inhibin activity, chemotactic/chemokinetic activity, hematopoietic
 XX and thrombolytic activity, receptor/ligand activity, anti-inflammatory
 XX activity, cadherin/tumor invasion suppressor activity, tumor inhibition
 XX therapy. The EST sequences are also stated to be useful for gene
 XX therapy.
 SQ Sequence 491 BP: 104 A: 137 C: 111 G: 138 T: 1 other:
 Query Match 0.38: Score 18: DB 20: Length 491.
 Best Local Similarity 100.0%: Pred. No. 3e+02:
 Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 3961 ggtttcaaaatttttttttt 3978
 DB 250 GCTTCCAAAATTCTTA 233
 RESULT 142
 XN 10-APR-1998: 98MO-0506954.
 XN X97675 standard: DNM: 507 BP.
 XN X97675:
 XN 13-SEP-1999 (first entry)
 XX

28-MAY-1998 (first entry)
 DE 3' nucleotide sequence of clone D305.2.
 XX
 XX D305.2 clone: cDNA library; cell proliferation; cell differentiation;
 XX as.
 XX Homo sapiens.
 XX Key location/Qualifiers
 XX P1 polyA signal 474..480
 XX P2 US708157-A.
 XX 13-JAN-1998.
 XX 26-JUL-1996: 9605-0686878.
 XX 26-JUL-1996: 9605-0686878.
 XX (GEM) GENETICS INST INC.
 XX (JACO) JACOBS K.

```

PI  Evans C, Jacobs K, Lavinia ER, McCoy JM, Herberg D:
PP  J Exp Med 1990;171:111-120.
PR  100%
PS  100%
DR  WPI: 1990-100352/10.
XX  Human testis derived cDNA and protein(s) - may be useful for
PP  reproductive use, or for stimulating cell proliferation and
PR  differentiation.
PS  Disclosure: Colton 63-62; 48PP: English.
XX  CC  This sequence is the 3' nucleotide sequence for the D305.2 clone, which
CC  is isolated from a human PBMC cDNA library. This clone has been
CC  was searched in the Genbank database, the clone demonstrated homology
CC  with an EST identified as "1191905: at Homo sapiens cDNA clone 139536 3'".
XX  Sequence 507 BP: 165 A: 70 C: 83 G: 189 T: 0 other;
DR  100%
XX  Query Match 0.38; Score 18; DB 19; Length 507;
XX  Percent Identity 100.0%; Pident No. 4e02; Indels 0; Gaps 0.
XX  Matches 18; Conservative 0; Mismatches 0.
XX  Oy 385 aaTgaaataaataaataaataa 402
XX  111111111111111111111111111111
XX  Db 490 aaGaaataaataaataaataa 507
XX  111111111111111111111111111111
XX  RESULT 143
XX  P35327 standard: cDNA, 507 BP.
XX  X77537 standard: cDNA, 507 BP.
XX  X77537:
XX  10-AUG-1999 (first entry)
XX  Human secreted protein D305.2 cDNA fragment 3.
XX  Secreted protein, testes; brain; blood; placenta; human; thymus;
XX  bone marrow; treatment; prevention; nutrition; cytokine;
XX  cell proliferation; cell differentiation; suppressor; tumour inhibition;
XX  hematopoietic; regulator; activin; inhibin; chemoketic; chemoketic;
XX  chemoketic; chemoketic; receptor; ligand; anti-inflammatory; tumour;
XX  suppressor; tumour invasion suppressor; gene therapy; tissue growth; as.
XX  Homo sapiens.
XX  W0939672-N1.
XX  P35327 standard: cDNA, 507 BP.
XX  X77537 standard: cDNA, 507 BP.
XX  X77537:
XX  10-AUG-1999.
XX  PD
XX  PD

```

Tue Mar 27 09:32:17 2001

us-09-410-035-4.011g.rng

Page 251

Tue Mar 27 09:32:17 2001

US-09-410-835-4.011g.rng

Page 252

```

SQ      Sequence 507 BP; 165 A; 70 C; 83 G; 189 T; 0 other;

Query Match      0.3%   Score 18; DB 21; Length 507;
      Beat Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps
DB      490 aatgcaaaaaaaaaaaaaa 507
      |||
RESULT 145
254438/C
ID      254438 standard; DNA; 516 BP.
AC      254438:
CT
PT      21-NM-2000 (first entry)
DT
DE      Neisseria gonorrhoeae ONP 925 partial DNA sequence SRO ID NO.2925.
FX
FX      Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
FX      antigenic; diagnostic; immunogenic; infection; meningitis; septicemia;
FX      antihemorrhagic; gene therapy; ds.
OS      Neisseria gonorrhoeae.
XX
XX      M09597200-42.
XX
PD      11-NOV-1999.
XX
XX      30-APR-1999: 99NM-05093146.
XX
XX      01-MAY-1998: 98US-0084758.
XX      11-JUL-1998: 98US-0094859.
XX      07-SEP-1998: 98US-0038934.
XX      07-SEP-1998: 98US-0095042.
XX      07-SEP-1998: 98US-0101268.
XX      09-OCT-1998: 98US-0103744.
XX      09-OCT-1998: 98US-0103766.
XX      25-FEB-1999: 99US-0121538.
XX
XX      (CHIR) CHIRON CORP.
XX      (GENO) INST GENOMIC RES.
XX
XX      Fraser C, Galavotti C, Grandi G, Hickey E, Manignani V, Mora M,
XX      Pizzi J, J., Neppolit R, Natti G, Scalzo E, Scarselli M,
XX      Tettolin H, Venter JC.
XX      WPI: 2000-062150/05.

```


Tue Mar 27 09:32:17 2001

us-09-410-835-4.01g.rng

Page 259

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.rng

Page 260

RESULT 151
 V02860 standard: cDNA: 566 BP.
 AC V02860:
 XX 11-MY-1998 (first entry)
 XX 11-MY-1998 (first entry)
 XX Human HMG1-C aberrant form 1.
 XX High mobility group protein: HMG1-C; MAC; human; treatment: modulator;
 XX multiple tumor aberration growth gene; vascular development;
 XX angiogenesis; vasculature; endometrial; contraception
 XX tissue regeneration; ss.
 XX Homo sapiens.
 XX DE1948122-A1.
 XX 26-JUN-1997.
 XX 21-DEC-1995: 950E-1048122.
 XX 21-DEC-1995: 950E-1048122.
 XX (BULL.) BULLERIKER J.
 XX Bullerik J.
 XX WPI: 1997-33387/31.
 XX DNA sequences representing aberrant forms of human high mobility
 XX group protein genes - useful for treatment of endometrial and
 XX tumor, or for modulating vasculature, etc.
 XX Claim 1: Fig 1: 58pp: German.
 XX V02860-V02868 are cDNA sequences that encode aberrant forms of the human
 XX high mobility group protein (HMG1-C) which is a member of the HMG1-C
 XX chromosome 11. These sequences encode the DNA binding part of the
 XX translation product but not the protein binding domain. These proteins,
 XX antitumor derived from these proteins or expression modulators of the
 XX HMG1-C gene, are used in the treatment of cancer. Such
 XX HMG1-C can reduce blood vessel permeability and inhibit tumor growth. Such
 XX HMG1-C can improve vascular function in myocardium damaged by infarction. Such
 XX proteins can also be used to treat endometrial and tumor, for
 XX contraception (local or oral) and for tissue regeneration, especially in
 XX the treatment of cancer. The HMG1-C gene can be used in a method for
 XX the treatment of cancer. The HMG1-C gene can be used in a method for
 XX use of biological material with attendant risks of viral transmission and

Tue Mar 27 09:32:17 2001

us-09-410-835-4.019.rmg

Page 263

PT DNA - antagonists and oligo-nucleotide(s), useful for modulating
 XX neuronal development and activity of motor and cholinergic neurons
 XX Example 7: Fig 11: 65pp: English.
 XX This is the nucleotide sequence of a rat EX clone. This encodes a
 XX protein of 110 amino acids. The protein is a member of the specific protein
 XX family. The protein is a member of the specific protein family. The
 XX LVI/haemophilin-7 sequence are used for screening and cloning beta-globin
 XX like sequences from rat cDNA library by PCR amplification. The
 XX protein is an agonist of the angiotensin IV receptor and is
 XX its endogenous ligand. The protein is a member of the specific protein
 XX family. The protein is a member of the specific protein family. The
 XX behavior and has vasoactive effects and can dilate cerebral arteries,
 XX increase renal blood flow and stereotypy behaviour, facilitate memory
 XX retrieval, induce neurite remodeling, and alleviate effects of spinal
 XX activity of motor neurons. The protein is a member of the specific protein
 XX family. The protein is a member of the specific protein family. The
 XX neurodegeneration (involving cholinergic, motor or sensory pathways),
 XX memory and motor peripheral neuropathy, brain injury and spinal cord
 XX disease). Antisense specific for the peptide can be used to determine
 XX its amount of in tissues and tissue regions.
 XX Sequence 613 BP: 159 A: 147 C: 155 G: 152 T: 0 other:
 XX
 XX Query Match 0.38: Score 18: DB 19: Length 613:
 XX Best Local Similarity 100.0%: Pred. No. 3e+02:
 XX Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 XX
 XX 53 cttggaatcgcgccta 70
 XX 551 cttggaatcgcgccta 568
 XX
 XX RESULT 153
 XX V06929 standard: cDNA: 634 BP.
 XX AC V06929:
 XX 27-APR-1999 (first entry)
 XX EST clone BR399.
 XX Expressed sequence tag: secreted protein: haematopoietic regulator;
 XX human; chemokine; chemokine; chemokine; chemokine; chemokine;
 XX receptor; ligand: anti-inflammatory; tumour inhibitor; ss.
 XX

Tue Mar 27 09:32:17 2001

us-09-410-835-4.019.rmg

Page 262

CC anaphylactic shock, is avoided.
 XX Sequence 566 BP: 186 A: 136 C: 140 G: 104 T: 0 other:
 XX
 XX Query Match 0.38: Score 18: DB 18: Length 566:
 XX Best Local Similarity 100.0%: Pred. No. 3e+02:
 XX Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 XX
 XX 385 aatgaaataaataaataa 402
 XX 544 aatgaaataaataaataa 561
 XX
 XX RESULT 152
 XX V03044 standard: DNA: 613 BP.
 XX AC V03044:
 XX 18-JUN-1998 (first entry)
 XX Rat EX clone nucleotide sequence.
 XX DE Rat EX clone nucleotide sequence.
 XX Angiotensin IV: neuroactive; Alzheimer's disease; modulator; dementia;
 XX neuronal development; vasodilator; neuropathy; brain injury;
 XX LVI/haemophilin-7; beta-globin; sheep; ss.
 XX Rattus sp.
 XX Key 2: location/Qualifiers
 XX PT CDS /tag= 0
 XX MO9801465-A1.
 XX 15-JAN-1998.
 XX 09-JUL-1997: 97MO-A000436.
 XX 09-JUL-1997: 96AU-0000893.
 XX (FLOR-) FLOREY INST EXPERIMENTAL PHYSIOLOGY.
 XX Aldred PG, Chai ST, Lev RA, Mendelsohn PA, Moller I,
 XX Smith JA.
 XX WPI: 1998-100995/09.
 XX P-PSDB: M37248.
 XX Neuro-active peptide with activities of angiotensin IV and related

Tue Mar 27 09:32:17 2001

us-09-410-835-4.019.rmg

Page 264

XX Homo sapiens.
 XX MO9845435-A2.
 XX 15-OCT-1998.
 XX 10-APR-1998: 98MO-0506954.
 XX 10-APR-1997: 97US-0835913.
 XX (GENV) GENETICS INST INC.
 XX Agostino MJ, Jacobs K, Lavelle ER, McCoy JM, Weisberg D,
 XX Moore DA, Spaulding V, Treacy M.
 XX WPI: 1999-070076/06.
 XX New polynucleotides encoding human secreted proteins - derived from
 XX cDNA libraries of human tissues and organs (e.g., placenta, brain,
 XX ovary, pituitary, retina and colon cDNA libraries).
 XX Claim 1: Page 395: 63pp: English.
 XX This sequence represents an expressed sequence tag (EST) and is a
 XX polynucleotide of the invention. The polynucleotide of the invention
 XX all secreted EST sequences and proteins encoded by them are predicted to
 XX be involved in the regulation of cell growth and differentiation. The
 XX treating, preventing or ameliorating medical conditions and
 XX animals, although no supporting data is given. Suggested activities
 XX include nutritional activity, immune stimulating or suppressing activity,
 XX angiogenesis, regulating activity, tissue growth activity, hematopoietic
 XX activity, neurotrophic activity, neurotrophic activity, neurotrophic
 XX activity, cadherin/tumour invasion suppressor activity, anti-inflam-
 XX matory activity. The EST sequences are also stated to be useful for gene
 XX therapy.
 XX Sequence 634 BP: 200 A: 114 C: 121 G: 198 T: 1 other:
 XX
 XX Query Match 0.38: Score 18: DB 20: Length 634:
 XX Best Local Similarity 100.0%: Pred. No. 3e+02:
 XX Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 XX
 XX 4346 tcttaagtcgacgacg 4363
 XX 504 tcttaagtcgacgacg 487
 XX
 XX RESULT 154

CC	of expression vectors and secretion vectors.
XX	Sequence 675 BP; 226 A; 97 C; 110 G; 242 T; 0 other;
OY	Query Match
PI	Best Local Similarity: 100.0%; Prid No. Jc020;
PI	Matches 18; Complementarity 0; Mismatches 0; Indels 0; Gaps 0;
DB	385 atgcagataaaaaaaaaaa 402 658 atcgaaaaaataaaaaaaa 675
RESULT 157	
XX	L16920/c
XX	L16920 standard cDNA, 676 BP.
AC	AC
XX	L16920:
XX	12-OCT-1999 (first entry)
DE	Human gene expression product cDNA sequence SPQ ID NO:4390.
XX	Homo sapiens
XX	tissue: testis
XX	Human gene expression product; diagnosis; therapy probe;
KM	described in patent application
XX	genetic analysis; colorectal cancer; breast cancer; lung cancer; aa.
XX	Homo sapiens.
XX	MO93B877-A2.
PN	PD
XX	05-AUG-1999.
PP	28-JAN-1999; 99MD-US01619.
XX	PR
XX	03-APR-1998; 98US-0080866.
XX	27-FEB-1998; 98US-0072830.
XX	27-FEB-1998; 98US-0072830.
PR	31-MAR-1998; 98US-0080114.
PR	03-APR-1998; 98PS-0080515.
XX	(CUR) CAPTOR CORP.
PA	(HRS-) HRSO INC.
XX	Grienvaklov R, Dickson M, Dmanac R, Dmanac S;
PI	Jacobsohn J, Garcia PO, Garcia V, Glase K, Inlita MU;
PI	Lasson G, Lebnovits D, Pos D, Randazzo E, Reinhard C,
PI	Stache-Crain B, Suduth-Klinger J, Williams LT;

```

DM  WPI: 1399-19400927.41.
XX
XX  Novel human genes and their expression products which are
XX  differentially expressed in different cell types
XX
XX  Claim 1: Page 2079, 2473pp: English.
XX
XX  The present invention describes a library of human polynucleotides
XX  corresponding to the sequences in 215522 to 21779. Also described is a
XX  method of detecting differentially expressed genes. The method
XX  comprises: (a) identifying a differentially expressed gene product in
XX  a cancerous state of a mammalian cell, comprising detecting at least one
XX  differentially expressed gene product in a test sample from a cell
XX  of a specific type of being cancerous, where the gene product is encoded by one
XX  or more polynucleotides; (b) identifying the polynucleotide sequence
XX  of the polynucleotides that can be used as a source of primers and probes, which can
XX  be used for a variety of purposes, e.g., detection of expression levels,
XX  mapping, tissue typing or profiling, formation, genetic analysis and
XX  identification of the gene product; (c) identifying the polynucleotides
XX  that can be used for raising antibodies for experimentally detecting
XX  therapeutic purposes. The polynucleotides may also be used to construct
XX  arrays for diagnostic (which may be used to determine function of an
XX  array of genes) or prognostic purposes. The polynucleotides may also
XX  be used for identifying the expression levels of the polynucleotides
XX  of two cells, e.g., to identify the differences in expression levels
XX  between a normal cell and a cancerous cell. The polynucleotides may
XX  identify a genetic predisposition or susceptibility to a disease such as
XX  cancer. The polynucleotides of the invention are especially used in the
XX  diagnosis, prognosis and management of colorectal cancer, breast cancer,
XX  and lung cancer. The polynucleotides of the invention can also be used to screen for
XX  peptide analogues and antagonists.
XX
XX  Sequence 676 BP; 184 A; 129 C; 144 G; 208 T; 10 other:
XX
XX  Query Match      0.3%; Score 18: DB 20; Length 676;
XX  Match Local Similarity 100.0%; Pctd Mo. Jct02;
XX  Mismatches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX  Db      385 attgcaaaaaaaaaaaaaa 402
XX      |||
XX      83 AATCCGAAAGAAAGAAAGAAAGAA 66
XX
XX  RESULT 158
XX  124068
XX  124068 standard: cDNA, 680 BP:
XX  AC  A25408:
XX  29-JUN-2000 (first entry)
XX  XX
XX  Human secreted protein gene 61 SEQ ID NO:73.
XX

```

Kw Human; secreted proteinase; diagenetic; cycloactive; immunosuppressive;
Kv inhibitory; antitumor; neuroprotection; neuroprotective; antiinfective;
Kt secretory; antiparasitic; antibacterial; antidiabetic; antisthma;
Ku antihelminthic; inflammatory; blood disorder; tumour; skin
Kx Immune disease; inflammation; blood disorder; tumour; skin
Xx Homo sapiens.
Mo020006698.v1.
Pn .
Px .
Py 10-FEB-2000.
Pz 23-JUL-1999: 99NM-USJ1730.
PR 10-JUL-1998: 98BS-0094657.
PR 10-AUG-1998: 98BS-0094657.
PR 06-AUG-1998: 98BS-0095456.
PR 06-AUG-1998: 98BS-0095455.
PR 12-AUG-1998: 98DS-0096319.
Px (HIV-) HUMAN GENE(S) SCI. INC.
P1 Komatsuoka CA, Rosen CA, Ruben SH, Duan R, Moore PA, Shi Y,
P2 Lattinud B, Wei T, N J, Florence DA, Young PE, Brewer LA;
P3 Doppel DR, Endresen GA, Ender R, Olsen HS, Muchnick M;
P4 WPI: 2000-195282/717.
Dr P-PSDB: YJ1533.
P7 New isolated human genes and the secreted polypeptides they encode.
P7 useful for diagnosis and treatment of e.g. cancer, neurological
P7 disorders, immune diseases, inflammation or blood disorders
Px .
Py .
Pz Claim 1: Page 416: 634pp: English.
Cc The polynucleotide sequence found in A26146 encode the human
Cc secreted proteins found in YJ1531 to YJ1631. The human secreted proteins
Cc Examples of the activities on the tissues and cells they are expressed in.
Cc antihelminthic; neurotoxic; neuroprotective; antiallergic; osteoprotective;
Cc antimetastatic; anticancer; antidiabetic; antisthma; antiparasitic;
Cc proinflammatory. The polynucleotides and their corresponding secreted
Cc products can be used for the diagnosis and treatment of various conditions,
Cc conditions, e.g. by protein or gene therapy. Also pathological conditions
Cc can be diagnosed by determining the amount of the proteins in a sample or
Cc tissue they are most highly expressed in.
Cc products for the diagnosis or treatment of cancer, tumours developing
Cc neurodegenerative disorders, developmental abnormalities and foetal
Cc deficiencies, blood disorders, diseases of the immune system.

```
CC autoimmune diseases, hepatic and renal diseases; inflammation,  
CC arteritis, Alzheimer's and behavioral disorders, ecchymosis,  
CC osteoporosis, arthritis, infections, AIDS, spinal cord injuries,  
CC transplants rejection, diabetes, asthma, sepsis acne, psoriasis,  
CC disorders, immunodeficiency, endometriosis, gonorrhea, genital  
CC disorders, respiratory disorders and metabolic disorders;  
or polyketoides can also be used as food additives or preservatives.  
CC The proteins are also useful for identifying their binding partners.  
CC present invention.
```

Sequence 680 BP: 163 A; 185 C; 167 G; 156 T; 9 other;

XX

SX Query Match 0.3% Score 18; DB ZI Length 680:
Best Local Similarity 100.0%; Pwd No. 3e-02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 385 atgcagcaaaaaaaaaaa 402
 |||||||
DB 615 atgacgaataaaaaaaa 652

RESULT 159

VZ4706
VZ4706 standard; DNM. 693 BP.

AC VZ4706:

TX 15-JUN-1998 (first entry)
TY
TZ H. pLori ORF 14ccl11orf3.

DE Cytoplasmic; replication; treatment; infection; envelope;
FM inhibitor; signaling compound; bacteria life cycle; activator;
SM inhibitor; dendritic virus disease; chronic gastritis; diagnosis; ds.
OS Helicobacter pylori.

PB

FH Location/OmitOffsets
FH Key /?tag = a
FT IDS 1..693
FX note= no stop codon given*

XN MO97J104-A1.

MX

PD 09-OCT-1997.

PE

PF 27-MAR-1997; 97NO-U0S0523.

PR 06 DEC 1996; 96DS-0761318.

DE	XN	
XX	Human gene expression product cDNA sequence SEQ ID NO:2612.	
XX		
XX	Human; gene; gene expression product; diagnosis; therapy; probe;	
KM	detection; mapping; tissue typing; proliferating; forensic; cancer;	
KM	genetic analysis; colorectal cancer; breast cancer; lung cancer; es-	
CC	ophagus.	
XX		
XX	Homoe sapiens.	
XX		
XX	M099387-7-42.	
XX		
XX	05-AUG-1999.	
XX		
XX	28-JAN-1999: 39MO-US01619.	
XX		
XX	03-APR-1998: 98MS-0080666.	
XX	03-APR-1998: 98MS-0075934.	
PR	24-FEB-1998: 98MS-0075934.	
PR	31-MAR-1998: 98MS-0080114.	
PR	01-APR-1998: 98MS-0080515.	
PA	(CHIR) CHIRON CORP.	
PA	(HRS) HERSO INC.	
XX		
XX	Crematovator R., Dickson M., Dmanac S.	
P1	Jones W.L., Kesham P., Kennedy C., Alesio R., Leung M.	
P1	Lamson G., Resnikoff D., Pot D., Randazzo P., Reinhard C.	
P1	Stecher-Grahn B., Sundtsh-Rittiger J., Williams Lf:	
D8	WPI: 1899-494092/41.	
XX		
P7	Novel human genes and their expression products which are	
XX	differentially expressed in different cell types	
XX		
PS	Claim 1: Page 1373: 2479p: English.	
XX		
XX	The present invention describes a library of human polynucleotides	
CC	comprising at least one nucleotide sequence having a length of 10 to 2,000 bp. Also described is a	
CC	method of detecting differentially expressed genes in a mammalian cell, comprising detecting at least one	
CC	differentially expressed gene product in a test sample from a cell	
CC	sample, said being cancerous, where the gene product is encoded by one	
CC	of the polynucleotides can be used as a source of primers and probes which can	
CC	be used for a variety of purposes, e.g. detection of expression levels,	
CC	tissue typing or profiling, forensic, genetic analysis and	
CC	diagnosis. The polynucleotides may also be used for diagnostic	
CC	therapeutic purposes. The polynucleotides may also be used to construct	
CC	arrays for diagnostics (which may be used to determine function of an	

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.png

Page 275

```
CC encoded protein), and to detect differences in expression levels between  
CC two cells (e.g. to identify abnormal or diseased tissue in a human, to  
CC cancer). The polynucleotides of interest are susceptible to a disease such as  
CC diagnosis, prognosis and management of colorectal cancer, breast cancer,  
CC peptide analogues. The polynucleotides can also be used to screen for  
XX sequence 742 BP; 158 A; 191 C; 156 G; 179 T; 16 other:  
  
Query Match 0.34 Score 18 DB 20 Length 742;  
Best Local Similarity 100.0% Positives 0 Mismatches 0 Gaps 0  
Matches 18 Conservative 0 Mismatches 0 Indels 0  
Db 682 Aatgataaaataaaaataa 402  
Oy 385 Aatgataaaataaaaataa 402  
Dd 682 Aatgataaaataaaaataa 699  
  
RESULT 163  
A17024  
A17024 standard: cDNA: 756 bp.  
Xx A17024:  
Dt 08-AUG-2000 (first entry)  
Xx human PRG01018 (UMC501) cDNA sequence SEQ ID NO:7.  
Dt Human: PRO polypeptide: amino acid sequence; receptor; diagnosis;  
Xx transmembrane; secretion; immunoadhesion; pharmaceutical; screening;  
Xx aa.  
Xx Homo sapiens.  
Xx MO100012708-A2.  
Pr 09-MAR-2000.  
Xx  
Xx  
Pf 01-SEP-1999: 99MO-US20111.  
Xx 01-SEP-1999: 98US-0098716.  
Pr 01-SEP-1999: 98US-0098716.  
Xx 01-SEP-1999: 98US-0098750.  
Pr 01-SEP-1999: 98US-0098803.  
Xx 01-SEP-1999: 98US-0098821.  
Pr 01-SEP-1999: 98US-0098839.  
Xx 01-SEP-1999: 98US-0099536.  
Pr 01-SEP-1999: 98US-0099536.  
Xx 01-SEP-1999: 98US-0099596.
```

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.rnd

Page 280

PR	09-SEP-1998	9805-0093602
PR	09-SEP-1998	9805-0093642
PR	09-SEP-1998	9805-0093711
PR	10-SEP-1998	9805-0093741
PR	10-SEP-1998	9805-0093763
PR	10-SEP-1998	9805-0093792
PR	10-SEP-1998	9805-0093808
PR	10-SEP-1998	9805-0093815
PR	10-SEP-1998	9805-0093815
PR	10-SEP-1998	9805-0093816
PR	15-SEP-1998	9805-0100135
PR	15-SEP-1998	9805-0100136
PR	15-SEP-1998	9805-0100138
PR	16-SEP-1998	9805-0100584
PR	16-SEP-1998	9805-0100627
PR	16-SEP-1998	9805-0100631
PR	16-SEP-1998	9805-0100644
PR	17-SEP-1998	9805-0100663
PR	17-SEP-1998	9805-0100684
PR	17-SEP-1998	9805-0100710
PR	17-SEP-1998	9805-0100710
PR	17-SEP-1998	9805-0100919
PR	17-SEP-1998	9805-0100930
PR	18-SEP-1998	9805-0100848
PR	18-SEP-1998	9805-0100848
PR	18-SEP-1998	9805-0101014
PR	18-SEP-1998	9805-0101068
PR	18-SEP-1998	9805-0101071
PR	18-SEP-1998	9805-0101279
PR	23-SEP-1998	9805-0101472
PR	23-SEP-1998	9805-0101474
PR	23-SEP-1998	9805-0101474
PR	23-SEP-1998	9805-0101475
PR	23-SEP-1998	9805-0101475
PR	23-SEP-1998	9805-0101475
PR	23-SEP-1998	9805-0101479
PR	24-SEP-1998	9805-0101718
PR	24-SEP-1998	9805-0101741
PR	24-SEP-1998	9805-0101741
PR	24-SEP-1998	9805-0101915
PR	24-SEP-1998	9805-0101916
PR	29-SEP-1998	9805-0102027
PR	29-SEP-1998	9805-0102030
PR	29-SEP-1998	9805-0102030
PR	29-SEP-1998	9805-0102310
PR	29-SEP-1998	9805-0102311
PR	30-SEP-1998	9805-0102484
PR	30-SEP-1998	9805-0102571
PR	30-SEP-1998	9805-0102571

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.png

Page 275

PR	01-OCT-1998	9805-0102684
PR	02-OCT-1998	9805-0102687
PR	03-OCT-1998	9805-0102685
PR	04-OCT-1998	9805-0102689
PR	05-OCT-1998	9805-0102695
PR	06-OCT-1998	9805-0103449
PR	07-OCT-1998	9805-0103314
PR	07-OCT-1998	9805-0103315
PR	07-OCT-1998	9805-0103328
PR	07-OCT-1998	9805-0103358
PR	07-OCT-1998	9805-0103366
PR	07-OCT-1998	9805-0103401
PR	08-OCT-1998	9805-0103613
PR	08-OCT-1998	9805-0103679
PR	08-OCT-1998	9805-0103711
PR	10-OCT-1998	9805-0104257
PR	12-OCT-1998	9805-0105007
PR	20-OCT-1998	9805-0105002
PR	21-OCT-1998	9805-0105104
PR	22-OCT-1998	9805-0105169
PR	22-OCT-1998	9805-0105693
PR	26-OCT-1998	9805-0105694
PR	27-OCT-1998	9805-0105807
PR	27-OCT-1998	9805-0105882
PR	27-OCT-1998	9805-0106062
PR	28-OCT-1998	9805-0106033
PR	28-OCT-1998	9805-0106039
PR	28-OCT-1998	9805-0106032
PR	28-OCT-1998	9805-0106033
PR	28-OCT-1998	9805-0106178
PR	29-OCT-1998	9805-0106340
PR	29-OCT-1998	9805-0106500
PR	10-OCT-1998	9805-0106464
PR	01-NOV-1998	9805-0106856
PR	01-NOV-1998	9805-0106905
PR	03-NOV-1998	9805-0106919
PR	03-NOV-1998	9805-0106932
PR	03-NOV-1998	9805-0106932
PR	03-NOV-1998	9805-0107261
PR	11-NOV-1998	9805-0108775
PR	17-NOV-1998	9805-0108779
PR	17-NOV-1998	9805-0108787
PR	17-NOV-1998	9805-0108801
PR	17-NOV-1998	9805-0108802

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.rnd

Page 280

XX 29-JUL-1997: 9705-0907615.
 PR 01-APR-1997: 9705-0831457.
 PR 24-JUN-1997: 9705-0881227.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (INMR) MERIEUX ORYAX PASTER MERIEUX SERUMS.
 XX A1-Garavi A, Kleinhous H, Miller C, Cohen RP, Tomb J;
 DR MPI: 1998-542393/46.
 PR P-PSDB: W98631.
 XX New isolated Helicobacter polynucleotides - used to develop products
 for diagnosis, prevention and treatment of Helicobacter
 PT infections and gastrointestinal diseases
 XX Claim 1: Page 1286-1287: 2054pp: English.
 XX This sequence represents a polynucleotide of the invention. It was
 CC isolated from Helicobacter pylori and encodes a protein that is useful
 CC for the prevention and treatment of Helicobacter infections.
 CC The polypeptides can be used for preventing or treating Helicobacter
 CC infections, including acute, chronic, and atrophic gastritis, and peptic
 CC ulcers, and for the production of antibodies. The products can also be used for
 CC detection and diagnosis.
 CC Sequence 810 BP: 258 A: 179 C: 157 G: 215 T: 1 other:
 SO
 Query Match 0.38; Score 18; DB 19; Length 810;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4528 ttttagagcaattgac 4545
 Db 335 ttttagagcaattgac 352
 RESULT 167
 V11433/C
 V11433 standard: cDNA: 811 BP.
 AC V11433;
 XX 23-JUL-1998 (first entry)
 PT Human secreted protein clone A1143_1 cDNA 3'-end.
 DE Secreted protein: prevention; treatment; gene therapy; ds.
 XX

Tue Mar 27 09:32:17 2001

us-09-410-835-4-ol19.rng

Page 267

XX Secreted protein: cancer; tumor; neurodegenerative disorder;
 KW developmental abnormality; fetal; deficiency; disease;
 KW CNS disorder; immune system disease; autoimmune disease; hepatic disease;
 KW renal disease; diabetes; inflammation; allergy; ischemic shock;
 KW prostate; cognitive disorder; schizophrenia; cardiovascular disorder;
 KW prostate disease; asthma; osteoporosis; arthritis; ds.
 XX Homo sapiens.
 OS
 XX M09507851-A1.
 XX 18-FEB-1999.
 PD 04-AUG-1998: 98MO-0516235.
 XX 19-AUG-1997: 97US-0056713.
 PR 05-AUG-1997: 97US-0054788.
 PR 05-AUG-1997: 97US-0054801.
 PR 05-AUG-1997: 97US-0054804.
 PR 05-AUG-1997: 97US-0054807.
 PR 05-AUG-1997: 97US-0054808.
 PR 05-AUG-1997: 97US-0054809.
 PR 05-AUG-1997: 97US-0055310.
 PR 05-AUG-1997: 97US-0055312.
 PR 05-AUG-1997: 97US-0055316.
 PR 05-AUG-1997: 97US-0055318.
 PR 05-AUG-1997: 97US-0055319.
 PR 05-AUG-1997: 97US-0055366.
 PR 05-AUG-1997: 97US-0056365.
 PR 05-AUG-1997: 97US-0056370.
 PR 05-AUG-1997: 97US-0056371.
 PR 05-AUG-1997: 97US-0056563.
 PR 05-AUG-1997: 97US-0056731.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Brewer LA, Ebnor R, Perle AM, Greene JM, Jandt F, Ji J;
 PT Olsen AS, Rosen CA, Rubin SM, Soppet DM, Young PE, Yu G;
 DR MPI: 1999-167452/14.
 PR P-PSDB: Y10873.
 XX New isolated human genes encoding secreted polypeptides - useful for
 PT diagnosis and treatment of pathological diseases
 XX Claim 3: Page 264: 33pp: English.
 PS

Tue Mar 27 09:32:17 2001

us-09-410-835-4-ol19.rng

Page 266

XX Homo sapiens.
 OS
 XX M09501554-A2.
 XX 15-JAN-1998.
 PD 07-JUL-1997: 97MO-0511976.
 PR 09-JUL-1996: 96US-0677231.
 XX (GENV) GENETICS INST INC.
 XX Bowman M, Evans C, Jacobs R, Lavalie RP, McCoy JM,
 PT Merberg D, Racie LA, Spaulding V, Treacy M;
 DR MPI: 1998-110230/10.
 PR P-PSDB: W98849.
 XX Secreted proteins and polynucleotides encoding them - useful to
 PT prevent, treat and ameliorate medical conditions
 XX Claim 25: Page 65-66: 93pp: English.
 CC V11433 and V11433 encode fragments of a novel secreted protein derived
 CC from clone A1143_1 which was isolated from a human adult testes cDNA
 CC library. The protein can be used to prevent, treat or ameliorate a
 CC medical condition, while the polynucleotides can be used for gene
 CC therapy.
 XX Sequence 811 BP: 210 A: 210 C: 166 G: 191 T: 34 other:
 SO
 Query Match 0.38; Score 18; DB 19; Length 811;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 3963 ggttcacaaatcttca 3978
 Db 448 ggttcacaaatcttca 431
 RESULT 168
 X30394
 X30394 standard: DNA: 840 BP.
 AC X30394;
 XX 14-MAY-1999 (first entry)
 PT DNA encoding a human secreted protein.
 DE
 XX

Tue Mar 27 09:32:17 2001

us-09-410-835-4-ol19.rng

Page 268

XX The specification describes secreted proteins and their corresponding
 CC polynucleotides which are useful for preventing, treating or ameliorating
 CC medical conditions, e.g. by protein or gene therapy, pathological
 CC conditions, e.g. by protein or gene therapy, pathological conditions,
 CC secreted polypeptides in a sample or by determining the amount of the
 CC mutations in the polynucleotides. Specific uses are described for each
 CC of the products, based on which tissues they are most highly
 CC expressed in. The products include secreted proteins for the diagnosis or
 CC treatment of cancer, immune system disorders, blood disorders, CNS disorders,
 CC abnormalities and foetal deficiencies, blood disorders, hepatic and renal
 CC diseases, diabetes, inflammation, allergy, cardiovascular disorders,
 CC prostate disease, asthma, osteoporosis, autoimmune disease, hepatitis
 CC osteoporosis, arthritis or malignancies, diseases of testes, lung or
 CC thymus, digestive/endocrine disorders, infections and AIDS. The
 CC polypeptides are also useful for identifying their binding partners.
 XX Sequence 840 BP: 256 A: 129 C: 166 G: 287 T: 2 other:
 SO
 Query Match 0.38; Score 18; DB 20; Length 840;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 385 atgtgataaataaataa 402
 Db 807 atgtgataaataaataa 824
 RESULT 169
 X87814
 X87814 standard: cDNA: 855 BP.
 AC X87814;
 XX 23-SEP-1999 (first entry)
 PT Human secreted protein encoding cDNA 82.
 DE
 XX Secreted protein: human; cytotoxic; thrombotic; osteoporosis; forensic;
 KW diagnostic; gene therapy; chromosome mapping; secretion; vector; ds.
 XX Homo sapiens.
 OS
 XX M09925825-A2.
 XX 27-MAY-1999.
 PD 11-NOV-1998: 98MO-1801862.
 PR

	PX	04-SEP-1986:	980S-008937J.
XZ	PR	17-OCT-1987:	97US-000662V.
XX	PI	17-DIC-1987:	98US-000193K.
XP	O9-FEB-1998:	98US-007412I.	
XR	13-AVR-1998:	98US-008156J.	
XS	10-AUG-1998:	98US-000611L.	
XA	(GEST) CPNSGT.		
ZP	Bouguetere L., Duclert A., Dumas Milne Edwards J.; MPI: 1999-31872/29. P-PMD: Y16130.		
ZT	Extended cDNAs encoding secreted proteins Example 28 : Page 148-149, 307pp; English.		
ZZ	CC X87813-X97906 represent extended CDNA's which encode novel human secreted polypeptides (aa 16159-16222) and which have cytototoxic, thrombotic and angiogenic activities (aa 16159-16222). They may also be used in diagnostic tests or as probes to obtain antibodies capable of binding to the secreted protein. They may also be used in diagnostic, forensic, gene therapy and chromosome mapping procedures. One also include design of expression vectors and secretion vectors.		
E0	Sequence 855 BP: 291 A: 137 C: 119 G: 288 T: 0 other: 		
QY	Query Match 0.3% Score 18: DB 20: Length 855: Beat Local Similarity 100.0% Pred.No. 2.e+021 Matches 18: Conservative 0: Mismatches 0: Indels 0: Caps 0		
DB	385 aaatgagaaaaaaaacccccccccc 402 iiiiiiiii		
D0	838aatggaaaaaaaaaaaaaacccccc 855		
RZ	RESULT 170 207553		
JD	207553 standard: cDNA: 661 bp.		
AC	207553:		
XX	01-DEC-1999: (first entry)		
D7	Maise glutathione-S-transferase encoding cDNA (clone CHM.PX0014.B1).		
KX	Maise: Glutathione S-Transferase; GST; enzyme; transgenic plant; NM catalyses detoxification herbicide xenobiotic; ss.		

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.rmg

Page 291

1	FM	Male: glutathione-S-transferase; GST: transgenic plant;
2	XX	herbicide: detoxification, herbicide tolerance; aa.
3	XX	See aays.
4	XX	
5	XX	
6	XX	
7	XX	
8	XX	
9	XX	
10	XX	
11	XX	
12	XX	
13	XX	
14	XX	
15	XX	
16	XX	
17	XX	
18	XX	
19	XX	
20	XX	
21	XX	
22	XX	
23	XX	
24	XX	
25	XX	
26	XX	
27	XX	
28	XX	
29	XX	
30	XX	
31	XX	
32	XX	
33	XX	
34	XX	
35	XX	
36	XX	
37	XX	
38	XX	
39	XX	
40	XX	
41	XX	
42	XX	
43	XX	
44	XX	
45	XX	
46	XX	
47	XX	
48	XX	
49	XX	
50	XX	
51	XX	
52	XX	
53	XX	
54	XX	
55	XX	
56	XX	
57	XX	
58	XX	
59	XX	
60	XX	
61	XX	
62	XX	
63	XX	
64	XX	
65	XX	
66	XX	
67	XX	
68	XX	
69	XX	
70	XX	
71	XX	
72	XX	
73	XX	
74	XX	
75	XX	
76	XX	
77	XX	
78	XX	
79	XX	
80	XX	
81	XX	
82	XX	
83	XX	
84	XX	
85	XX	
86	XX	
87	XX	
88	XX	
89	XX	
90	XX	
91	XX	
92	XX	
93	XX	
94	XX	
95	XX	
96	XX	
97	XX	
98	XX	
99	XX	
100	XX	
101	XX	
102	XX	
103	XX	
104	XX	
105	XX	
106	XX	
107	XX	
108	XX	
109	XX	
110	XX	
111	XX	
112	XX	
113	XX	
114	XX	
115	XX	
116	XX	
117	XX	
118	XX	
119	XX	
120	XX	
121	XX	
122	XX	
123	XX	
124	XX	
125	XX	
126	XX	
127	XX	
128	XX	
129	XX	
130	XX	
131	XX	
132	XX	
133	XX	
134	XX	
135	XX	
136	XX	
137	XX	
138	XX	
139	XX	
140	XX	
141	XX	
142	XX	
143	XX	
144	XX	
145	XX	
146	XX	
147	XX	
148	XX	
149	XX	
150	XX	
151	XX	
152	XX	
153	XX	
154	XX	
155	XX	
156	XX	
157	XX	
158	XX	
159	XX	
160	XX	
161	XX	
162	XX	
163	XX	
164	XX	
165	XX	
166	XX	
167	XX	
168	XX	
169	XX	
170	XX	
171	XX	
172	XX	
173	XX	
174	XX	

XX	OS	Zea mays.
XX	FN	U85692229-A.
XX	DP	05-OCT-1999.
XX	PF	05-SEP-1997; 97US-0924759.
XX	PR	05-SEP-1997; 97US-0924759.
XX	(DUMP)	DOI POINT DE NEGOCIES & CO P.I.
XX	P1	McGonigle B., O'Keefe DP:
XX	NB	PL 1999-571265/48.
XX	DR	P-FSDBI: Y105481.
XX	PP	
XX	F7	Maise glutathione S-transferases
XX	FP	Claim 2; Columns 43-44; 30pp: English.
XX	CC	The invention provides isolated nucleic acid sequences encoding maize
XX	CC	glutathione S-transferase (GST) enzymes. The nucleic acid sequences are
XX	CC	GST cDNAs producing transgenic plants which express increased levels of
XX	CC	antioxidants. Sequences (407516-571) represent nucleotide sequence of
XX	CC	various cDNA clones encoding maize GST enzymes (Y40560-571).
XX	A0	Sequence 861 BP; 193 A; 291 C; 243 G; 114 T; 0 other;
XX	Query Match	0 JN; Score 18; DB 70; Length 861;
XX	Local similarity	100.0%; Pred. No. 2;e+00; Indels 0; Gaps 0;
XX	Matched 18; Conservative 0; Identical 0;	
QY	385 aa gaaataaaaaaaa 402	
DB	iiiiiiiii	
	829 acgtgaataaaaaaaga 846	
RESULT 171		
ID	1715284793 standard; cDNA; 661 bp.	
AC	294793;	
XX	01-MC-2000 (first entry)	
XX	Maise class III glutathione-S-transferase cDNA.	

Tue Mar 27 09:32:17 2001

us-09-410-035-4-011g.rmg

Page 292

Query Match	Score	18:	DB	21:	Length	861:
Best Local Similarity	100.0%					
Matches	18:	Conservative	0:	Mismatches	0:	Indels
	0:	Gaps	0:			
DB	365	atgagataaaaaaaaaa	402			
	829	atgagataaaaaaaaaa	846			
RESULT	172					
172113	172113	standard: cDNA to mRNA;	862	BP.		
AC	772173					
XX	25-FEB-1998	(first entry)				
XX	Alzheimer's disease	DNA sequence from plasmid pCCS1180.				
XX	Human: brain; Alzheimer's disease;	diagnosis: antibody; expression; ds.				
XX	Homio sapienta.					
XX	Key	Location/Qualifiers				
XX	CD5	772173				
XX	772173	772173				
XX	/note=	"Protein encoded by DNA from the human brain which has different expression from the normal protein when in an Alzheimer's disease patient."				
XX	MO9721807-AL.					
XX	19-JUN-1997.					
XX	12-DEC-1996;	96NO-JP01630.				
XX	12-DEC-1995;	95JP-0132745.				
XX	(RTOW) RTOW	HAKIO NOTO K.				
XX	Hashida H, Kuga T, Nakagawa S, Sakaki Y, Zhao N,					
XX	WPI: 1997-133779/30.					
XX	P-PDB: 013950.					
XX	Claim 3: Page 48-49: 90pp: Japanese.					
XX	The present sequence represents a DNA fragment which is complementary to					

RESULT 176
 ID 297102 standard: cDNA: 990 BP.
 XX 297102:
 XX 19-APR-2000 (first entry)
 DT
 OR Human secreted protein gene 94 cDNA clone HEBD40, SEQ ID NO:94.
 CC Human secreted protein; cancer; tumour; developmental abnormality;
 CC focal deficiency; blood disorder; immune system disorder; inflammation;
 CC autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 CC anisotropy; arthritis; aschias; psoriasis; aspsia; skin disorder;
 CC digestive disorder; endocrine disorder; infection; AIDS; leukemia;
 CC therapy; ds.
 XX Homo sapiens.
 XX MO966041-A1.
 PR 23-DEC-1999.
 XX 15-JUN-1999: 9960-US13418.
 XX 16-JUN-1998: 9805-0089507.
 XX 16-JUN-1998: 9805-0089508.
 XX 16-JUN-1998: 9805-0089509.
 XX 22-JUN-1998: 9805-0089510.
 XX 22-JUN-1998: 9805-0089511.
 XX 22-JUN-1998: 9805-0089512.
 XX (HUMA-) HUMAN GENE: ACT INC.
 XX Ribon SM, Ni J, Rosen CA, Mei Y, Young PE, Florence KA,
 XX Soppet DR, Brewer LA, Endress CA, Carter KC, Muenst M, Ehmer R,
 XX Lafleur DR, Olsen HS, Shi Y, Moore PA, Komatsoulis G:
 XX WPI: 2000-106100/09.
 DR P-PSDB: Y86398.
 XX New isolated human genes and the secreted polypeptides they encode,
 XX useful for diagnosis of various hematological
 XX disorders, immune diseases, inflammation or blood disorders.
 XX Claim 1: Page 367, 586pp: English.
 CC 297019 to 297137 represent 94 isolated human secreted protein genes.
 CC Y86315 to Y86333 are the secreted proteins encoded by the 94 human genes.
 CC This sequence represents a fragment of one of the human secreted

Tue Mar 27 09:32:17 2001

us-09-410-835-4-ol19.mg

Page 299

exon 186..1002
 /tag= c
 /number= 2
 P1 POLY_A_signal 962..967
 P2 /tag= d
 P3 MO9925736-A1.
 PD 27-MAY-1999.
 XX 13-NOV-1998: 98MD-0020052.
 XX 13-NOV-1997: 97MD-0004162.
 PR (RANO-) KAROLINSKA INNOVATIONS AB.
 P1 Einhorn S, Grander D, Liu Y, Oester D, Ranaol O,
 P1 Fabrovsky E:
 P1 WPI: 1999-11796/28.
 DR P-PSDB: Y86318.
 XX Chronic lymphocytic leukemia nucleotides and proteins
 XX Claim 5: Page 58-59: 81pp: English.
 CC This sequence represents human Leu1 (leukemia associated gene 1)
 CC cDNA. Previous studies had indicated the presence of a putative
 CC tumor suppressor gene on chromosome 13q14, commonly deleted in
 CC human leukemia. This gene, designated as leukemia (B-CLL), in
 CC the present invention, the human leukemia (B-CLL) gene, was
 CC narrowed to a 10 kb area, and 2 neighboring genes, termed Leu1
 CC and Leu2 (see X85801), that span this region have been identified,
 CC with several patients showing deletion borders within these
 CC genes. The human leukemia (B-CLL) gene was previously
 CC published genes at the nucleotide and protein level. The Leu1 and Leu2
 CC acid sequence level. Mutational analysis of the Leu1 and Leu2
 CC genes in 170 CLL samples revealed no small intragenic mutations or
 CC deletions. However, in all cases of 13q14 loss examined,
 CC the Leu1 and Leu2 genes were deleted. Thus, Leu1 and Leu2 are strong candidate tumor
 CC suppressor genes involved in B-CLL leukemogenesis. The invention
 CC relates to B-CLL associated nucleic acid and amino acid sequences,
 CC production of protein nucleic acid and amino acid sequences,
 CC for the diagnosis and treatment of B-CLL leukemia and other malignancies
 CC against leukemia and other malignancies of the same genetic area,
 CC for raising antibodies, and in diagnostic kits.
 CC Sequence 1002 BP: 288 A: 207 C: 216 G: 291 T: 0 other:

Tue Mar 27 09:32:17 2001

us-09-410-835-4-ol19.mg

Page 298

proteins. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions,
 CC for diagnosing or detecting the presence of a pathological condition, can be
 CC diagnosed by determining the amount of the secreted protein. Specific
 CC or by determining the presence of mutations in the new genes. Specific
 CC uses are described for each of the 94 genes, based on which tissues they
 CC are most highly expressed in, and include developing products for the
 CC diagnosis, treatment, prevention, and prognosis of various diseases,
 CC and focal deficiencies, blood disorders, inflammation, allergies, and cognitive
 CC autoimmune diseases, inflammation, allergies, psoriasis, aspsia, skin
 CC disorders, anisotropy, diabetes, cardiovascular disorders, kidney
 CC disease, digestive disorder, endocrine disorder, infection, AIDS, leukemia,
 CC polypeptides are also useful for identifying the B-CLL antigen. The
 CC The sequences shown in Y86314 to Y86585 represent fragments of the
 CC secreted proteins.
 XX Sequence 990 BP: 273 A: 259 C: 191 G: 261 T: 6 other:
 Query Match 0.34: Score 18: DB 21: Length 990:
 Best Local Similarity 100.0%: Pred No. 2: seq02:
 Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Or 389 aaaaaaaaaaaaaatgct 406
 Db 806 aaaaaaaaaaaaaatgct 823
 ||||||||||||||||
 RESULT 177
 ID 297103 standard: cDNA: 1002 BP.
 XX 297103:
 XX 16-AUG-1999 (first entry)
 DE Human leukemia-associated gene 1 (Leu1) cDNA.
 XX Leu1 gene; leukemia-associated gene 1; human; B-CLL;
 XX human leukemia; chronic lymphocytic leukemia; tumour suppressor;
 XX diagnosis; therapy; ds.
 XX Homo sapiens.
 XX Key 262..489
 XX CDS 1..389
 XX /tag= a
 XX /tag= b
 XX /number= 1
 P1 exon
 P2 /tag= a
 P3 /tag= b
 P4 /number= 1

Tue Mar 27 09:32:17 2001

us-09-410-835-4-ol19.mg

Page 300

Query Match 0.34: Score 18: DB 20: Length 1002:
 Best Local Similarity 100.0%: Pred No. 2: seq02:
 Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Or 385 aaaaaaaaaaaaaaaa 402
 Db 977 aatgaaaaaaaaaaaaaa 994
 ||||||||||||||||
 RESULT 178
 ID 297104 standard: DNA: 1047 BP.
 XX 297104:
 XX A08124:
 XX 27-JUN-2000 (first entry)
 DE C. trachomatis MOMP containing fusion protein nucleotide sequence 15.
 XX Chlamydia trachomatis; fusion protein; major outer membrane protein;
 XX MOMP; hydrophilic polypeptide; antibody; detection; diagnosis;
 XX infection; infectious disease; ds.
 XX Chlamydia trachomatis.
 XX Synthetic.
 XX Key 1..1047
 XX CDS 1..1047
 XX /tag= a
 XX /tag= b
 XX /note= "fusion protein containing at least part of a
 XX major outer membrane protein (MOMP) of Chlamydia
 XX trachomatis: no stop codon given"
 XX JP2000041678-A.
 PR 15-FEB-2000.
 PD 28-JUL-1998: 98JP-021312.
 XX 28-JUL-1998: 98JP-021312.
 PR (ELSD) DENKI KAKAO KOCIO KK.
 XX WPI: 2000-295780/26.
 DR P-PSDB: Y83397.
 XX A soluble fused protein useful for diagnosis of Chlamydia infection,
 XX comprises at least part of major outer membrane protein (MOMP) of
 XX Chlamydia trachomatis.
 XX Claim 20: Page 29-30: 37pp: Japanese.

XX The present invention describes fusion proteins (1) comprising at least
 CC part of a major outer membrane protein (MOMP) of Chlamydia trachomatis,
 CC secreted one hydrophilic polypeptide having no immunoreactivity to
 CC human serum, and a second polypeptide having immunoreactivity to
 CC specifically claimed examples of the fusion proteins given in 192386 to
 CC 182393. Also described is a method (A) for the detection of Chlamydia
 CC trachomatis antibody using (1) as the antigen. (1) is used for the
 CC detection of Chlamydia trachomatis infections diseases. The method can
 CC diagnose Chlamydia trachomatis infections diseases specifically in a
 CC high sensitivity.

SQ Sequence 1047 BP: 315 A: 200 C: 233 G: 290 T: 0 other:

Query Match 0.38: Score 18: DB 21: Length 1047:

Best Local Similarity 100.0%: Pred. No. 2.9e+02: Mismatches 0: Gaps 0:

Matches 10: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

DB 504 catcacatcacatca 521

RESULT 179

004287

ID 004287 standard: DNA: 1051 BP:

AC 004287:

UT 17-SEP-1990 (first entry)

DX Sequence encoding bovine trophoblast protein-1 (bTP-1) derived from

DE clone Lambda bTP509.

XX Bovine trophoblast protein-1: bTP-1; fertility: ds.

XX Sus scrofa.

XX EP67063-A.

XX 09-MAY-1990.

XX 23-OCT-1989: 89EP-0119642.

XX 26-OCT-1988: 88US-0262870.

XX (UNOR) UNIV OF MISSOURI.

PI Robert M. Imakawa K.

Tue Mar 27 09:32:17 2001

us-09-410-835-4-0119.rmg

Page 303

XX (UNOR) UNIV OF MISSOURI.
 XX Robert M. Imakawa K.
 XX WPI: 1990-141062/19.
 XX P-PSDB: R04539.
 XX Recombinant bovine trophoblast protein-1 -
 XX used for enhancing fertility or treating viral diseases in
 XX mammals, esp. cattle.
 XX Claim 3: Fig 1: 27pp: English.
 CC The bTP-1 produced from the gene may be used to promote fertility
 CC or treat viral disease in cattle. The gene may also be used to
 CC provide transgenic animals with enhanced fertility, or to
 CC prophylactic and therapeutic treatment of other mammals.
 SQ Sequence 1057 BP: 294 A: 260 C: 229 G: 274 T: 0 other:

Query Match 0.38: Score 18: DB 11: Length 1057:

Best Local Similarity 100.0%: Pred. No. 2.9e+02: Mismatches 0: Gaps 0:

Matches 10: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

DB 1033 atggaataataataata 1050

RESULT 181

ID 200410 standard: cDNA: 1080 BP.

AC 200410:

UT 04-OCT-1999 (first entry)

DX Human secreted protein cDNA encoding gene 1.

CC secreted protein: human; treatment: diagnosis; therapy; cancer; tumor;
 CC neurodegenerative disorder; developmental abnormality; blood disorder;
 CC fetal deficiency; blood disorder; leukemia; immune system; inflammation;
 CC autoimmune disease; hepatic disease; renal disease; allergy; testostona;
 CC cardiovascular disorder; wound healing; stroke; asthma; sepsis; acute;
 CC metabolic disorder; ss.

XX Homo sapiens.

Tue Mar 27 09:32:17 2001

us-09-410-835-4-0119.rmg

Page 302

DR WPI: 1990-141062/19.
 XX Recombinant bovine trophoblast protein-1 -
 XX used for enhancing fertility or treating viral diseases in
 XX mammals, esp. cattle.
 XX Disclosure: P: English.
 CC The bTP-1 produced from the gene may be used to promote fertility
 CC or treat viral disease in cattle. The gene may also be used to
 CC provide transgenic animals with enhanced fertility, or to
 CC prophylactic and therapeutic treatment of other mammals.
 CC See also R04286 and R04288.

SQ Sequence 1051 BP: 291 A: 258 C: 228 G: 274 T: 0 other:

Query Match 0.38: Score 18: DB 11: Length 1051:

Best Local Similarity 100.0%: Pred. No. 2.9e+02: Mismatches 0: Gaps 0:

Matches 10: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

DB 1030 atggaataataataata 1047

RESULT 180

004285

ID 004285 standard: cDNA: 1057 BP.

AC 004285:

UT 17-SEP-1990 (first entry)

DX cDNA clone of sequence encoding bovine trophoblast protein-1 (bTP-1).

XX Bovine trophoblast protein-1: bTP-1; fertility: ds.

XX Sus scrofa.

XX EP67063-A.

XX 09-MAY-1990.

XX 23-OCT-1989: 89EP-0119642.

XX 26-OCT-1988: 88US-0262870.

Tue Mar 27 09:32:17 2001

us-09-410-835-4-0119.rmg

Page 304

XX W0933801-11.
 XX 05-AUG-1999.
 XX 27-JAN-1999: 99NO-0501621.
 XX 30-JAN-1998: 98US-0073170.
 XX 30-JAN-1998: 98US-0073159.
 XX 30-JAN-1998: 98US-0073160.
 XX 30-JAN-1998: 98US-0073161.
 XX 30-JAN-1998: 98US-0073162.
 XX 30-JAN-1998: 98US-0073163.
 XX 30-JAN-1998: 98US-0073164.
 XX 30-JAN-1998: 98US-0073165.
 XX 30-JAN-1998: 98US-0073167.
 XX (HUMAN) HUMAN GENE SCT INC.
 XX Carter KC, Endress GA, Feng P, Ferlie AM, Florence C,
 XX Florentine MA, Janat P, Ni J, Rosen CA, Ruben SM,
 XX Doppet DM, Young P, Tu G.
 XX WPI: 1999-469315/39.
 XX P-PSDB: Y25711, Y25719.
 XX New isolated human genes and the secreted polypeptides they encode
 XX useful in, e.g. treatment of Alzheimer's

Claim 1a: Page 255-256: 39pp: English.

CC This invention describes novel human genes (see 200410-200417) and the
 CC secreted proteins (see Y25711-Y25719) and fragments (see Y25719-Y25707)
 CC they encode. The polynucleotides and their corresponding secreted
 CC polypeptides are useful for preventing, treating or ameliorating medical
 CC conditions associated with Alzheimer's disease, including the use of the
 CC gene or protein in the diagnosis, prognosis, or treatment of the disease.
 CC can be diagnosed by determining the presence of mutations in the new
 CC polynucleotides. Specific uses are described for each of the 67
 CC polynucleotides of the invention based on which tissues they are most
 CC highly expressed in and which diseases they are associated with.
 CC treatment of cancer, tumour, neurodegenerative disorders, developmental
 CC abnormalities and fetal deficiencies, blood disorders, hepatic and renal
 CC diseases of the immune system, autoimmune diseases, leukemia, and
 CC congenital disorders, achilophrenia, testostona, cardiovascular disorders,
 CC wound healing, stroke, arthritis, obesity, asthma, sepsis, acute,
 CC prostatic, transplant rejection, metabolic disorders, infections, AIDS,
 CC and other diseases. The polypeptides are also useful for identifying their binding
 CC partners.

Db 1160 aatgagagagagagagagagagag 1177
 |||
 RESULT 187
 ID A37072 standard: cDNA: 1204 BP.
 AC A37072:
 AT 08-AUG-2000 (first entry)
 DE Human PRO1279 (UNC649) cDNA sequence SEQ ID NO:169.
 XX
 XX Human: PRO polypeptide; membrane bound protein; receptor; diagnosis;
 KW transmembrane; secretion; immunomodulation; pharmaceutical; screening;
 ##
 OS Homo sapiens.
 PN NC0200012708-A2.
 PD 09-MAR-2000.
 XX
 XX 01-SEP-1999: 99MC-0520111.
 PR 01-SEP-1999: 98US-0098716.
 PR 01-SEP-1999: 98US-0098749.
 PR 01-SEP-1999: 98US-0098750.
 PR 02-SEP-1999: 98US-0098801.
 PR 02-SEP-1999: 98US-0098841.
 PR 09-SEP-1999: 98US-0099316.
 PR 09-SEP-1999: 98US-0099356.
 PR 09-SEP-1999: 98US-0099402.
 PR 09-SEP-1999: 98US-0099442.
 PR 10-SEP-1999: 98US-0099741.
 PR 10-SEP-1999: 98US-0099792.
 PR 10-SEP-1999: 98US-0099808.
 PR 10-SEP-1999: 98US-0099812.
 PR 10-SEP-1999: 98US-0099813.
 PR 15-SEP-1999: 98US-0100185.
 PR 15-SEP-1999: 98US-0100388.
 PR 15-SEP-1999: 98US-0100389.
 PR 15-SEP-1999: 98US-0100627.
 PR 16-SEP-1999: 98US-0100661.
 PR 16-SEP-1999: 98US-0100661.

Tue Mar 27 09:32:17 2001

us-09-410-835-4.0119.mrg

Page 315

PR 20-OCT-1998: 98US-0104987.
 PR 20-OCT-1998: 98US-0105000.
 PR 20-OCT-1998: 98US-0105010.
 PR 21-OCT-1998: 98US-0105104.
 PR 22-OCT-1998: 98US-0105169.
 PR 22-OCT-1998: 98US-0105266.
 PR 26-OCT-1998: 98US-0105691.
 PR 26-OCT-1998: 98US-0105807.
 PR 27-OCT-1998: 98US-0105881.
 PR 27-OCT-1998: 98US-0105882.
 PR 28-OCT-1998: 98US-0106023.
 PR 28-OCT-1998: 98US-0106039.
 PR 28-OCT-1998: 98US-0106310.
 PR 28-OCT-1998: 98US-0106312.
 PR 28-OCT-1998: 98US-0106313.
 PR 29-OCT-1998: 98US-0106348.
 PR 29-OCT-1998: 98US-0106384.
 PR 29-OCT-1998: 98US-0106500.
 PR 30-OCT-1998: 98US-0106556.
 PR 03-NOV-1998: 98US-0106592.
 PR 03-NOV-1998: 98US-0106905.
 PR 03-NOV-1998: 98US-0106932.
 PR 03-NOV-1998: 98US-0106934.
 PR 10-NOV-1998: 98US-0107193.
 PR 11-NOV-1998: 98US-0107175.
 PR 17-NOV-1998: 98US-0108775.
 PR 17-NOV-1998: 98US-0108788.
 PR 17-NOV-1998: 98US-0108801.
 PR 17-NOV-1998: 98US-0108806.
 PR 17-NOV-1998: 98US-0108807.
 PR 17-NOV-1998: 98US-0108867.
 PR 17-NOV-1998: 98US-0108875.
 PR 18-NOV-1998: 98US-0108845.
 PR 18-NOV-1998: 98US-0108849.
 PR 18-NOV-1998: 98US-0108850.
 PR 18-NOV-1998: 98US-0108851.
 PR 18-NOV-1998: 98US-0108852.
 PR 18-NOV-1998: 98US-0108858.
 PR 18-NOV-1998: 98US-0108904.
 XX (GENE) GENE/TECH INC.
 XX Baker K. Goddard A. Gurney AL. Smith V. Watanabe CK. Wood WT.
 PI
 XX

Tue Mar 27 09:32:17 2001

us-09-410-835-4.0119.mrg

Page 316

PR 16-SEP-1998: 98US-0100662.
 PR 16-SEP-1998: 98US-0100664.
 PR 16-SEP-1998: 98US-0100684.
 PR 17-SEP-1998: 98US-0100710.
 PR 17-SEP-1998: 98US-0100711.
 PR 17-SEP-1998: 98US-0100719.
 PR 17-SEP-1998: 98US-0100810.
 PR 18-SEP-1998: 98US-0100848.
 PR 18-SEP-1998: 98US-0100849.
 PR 18-SEP-1998: 98US-0101014.
 PR 18-SEP-1998: 98US-0101066.
 PR 18-SEP-1998: 98US-0101074.
 PR 23-SEP-1998: 98US-0101279.
 PR 23-SEP-1998: 98US-0101471.
 PR 23-SEP-1998: 98US-0101472.
 PR 23-SEP-1998: 98US-0101474.
 PR 23-SEP-1998: 98US-0101475.
 PR 23-SEP-1998: 98US-0101476.
 PR 23-SEP-1998: 98US-0101477.
 PR 24-SEP-1998: 98US-0101479.
 PR 24-SEP-1998: 98US-0101741.
 PR 24-SEP-1998: 98US-0101743.
 PR 24-SEP-1998: 98US-0101744.
 PR 24-SEP-1998: 98US-0101915.
 PR 24-SEP-1998: 98US-0101916.
 PR 25-SEP-1998: 98US-0102207.
 PR 25-SEP-1998: 98US-0102210.
 PR 25-SEP-1998: 98US-0102307.
 PR 25-SEP-1998: 98US-0102310.
 PR 25-SEP-1998: 98US-0102311.
 PR 25-SEP-1998: 98US-0102313.
 PR 25-SEP-1998: 98US-0102484.
 PR 25-SEP-1998: 98US-0102485.
 PR 30-SEP-1998: 98US-0102570.
 PR 30-SEP-1998: 98US-0102571.
 PR 01-OCT-1998: 98US-0102684.
 PR 01-OCT-1998: 98US-0102687.
 PR 02-OCT-1998: 98US-0102689.
 PR 06-OCT-1998: 98US-0103258.
 PR 06-OCT-1998: 98US-0103259.
 PR 07-OCT-1998: 98US-0103314.
 PR 07-OCT-1998: 98US-0103315.
 PR 07-OCT-1998: 98US-0103328.
 PR 07-OCT-1998: 98US-0103395.
 PR 07-OCT-1998: 98US-0103396.
 PR 07-OCT-1998: 98US-0103401.
 PR 07-OCT-1998: 98US-0103411.
 PR 08-OCT-1998: 98US-0103678.
 PR 08-OCT-1998: 98US-0103679.
 PR 14-OCT-1998: 98US-0103711.
 PR 14-OCT-1998: 98US-0104257.

Tue Mar 27 09:32:17 2001

us-09-410-835-4.0119.mrg

Page 316

DR WPI: 2000-317871/20.
 PR P-PSDB: Y93390.
 XX New mammalian DNA sequences encoding transmembrane, receptor or
 XX potential peptide or small molecule inhibitors of the relevant
 XX small molecule inhibitors of the relevant receptor/ligand interactions
 XX
 PS Claim 2: Fig 101: 773pp: English.
 CC A37072 to A37144 encode the new isolated human transmembrane, receptor
 CC or secreted PRO polypeptides given in Y9310 to Y9316 to Y9317 to Y9318
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding these proteins are also disclosed. The polypeptides and nucleotide
 CC pharmaceutical and diagnostic agents A37145 to A37173 including uses as
 CC PCR primers and hybridization probes used in the isolation of the PRO
 CC polypeptides from the present invention.
 SS Sequence 1204 BP: 364 A: 364 C: 294 G: 240 T: 0 other:
 50
 Query Match 0.3% Score 18: DB 21: Length 1204:
 Matches 18: Conservative 0: P: 0: N: 2: A: 0: T: 0: G: 0: C: 0: Indels 0: Gaps 0:
 Oy 385 aatgagagagagagagagagagag 402
 Db 1163 aatgagagagagagagagagagag 1180
 |||
 RESULT 188
 ID A37523 standard: cDNA: 1223 BP.
 AC A37523:
 AT 08-DEC-1999 (first entry)
 DE Human prostate cancer-associated EST 47.
 XX
 XX Expressed sequence tag: EST: prostate; tumor; treatment; gene therapy;
 KW cancer; tissue specificity; human; ds.
 OS Homo sapiens.
 PN DE19811194-A1.
 PD 16-SEP-1999.
 XX
 XX 10-MAR-1998: 98DE-1011194.

PR 31-JUL-1996; 96CA-2182421.
 XX (TOOH) UNIV QUEENS KINGSTON.
 XX Lefebvre DD, Malboobi MA.
 PI WPI: 1998-159169/14.
 DR P-PSDB: W56020.
 XX
 PT New isolated phosphate starvation-inducible genes - used to develop
 PT plants or other photosynthetic organisms with altered phosphorus
 PT metabolism, e.g. to alter growth or reproduction.
 XX
 XX Claim 2: Fig 5: 133pp: English.
 CC The present sequence encodes a phosphate starvation-induced protein
 CC kinase from a photosynthetic organism. In which transcription of the
 CC DNA is induced by phosphate deficiency. The products and methods of
 CC the invention are useful for developing plants or other photosynthetic
 CC organisms with altered phosphorus metabolism, e.g. to alter growth or
 CC reproduction, metabolic content, flowering, drought or cold tolerance
 CC or nutritive value.
 XX
 SD Sequence 1250 BP: 428 A; 206 C; 269 G; 347 T; 0 other:
 Query Match 0.3%; Score 18; DB 19; Length 1250;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 385 atgagagagagagagagagag 402
 Db 1232 atgagagagagagagagagag 1249
 RESULT 192
 T43482/C
 XX T43482 standard: DMN: 1254 BP.
 AC T43483;
 XX
 XX 11-NOV-1997 (first entry)
 DE ATM gene exons 48-49.
 XX
 XX ATM gene: ataxia-telangiectasia; progressive genetic disorder; antibody;
 XX central nervous system; immune system; chromosomal instability; therapy;
 XX multi-system disease; autosomal recessive; cerebellar ataxia;
 XX general motor dysfunction; Purkinje cells; oculocutaneous telangiectasia;
 XX blood vessels; bulbar conjunctiva; facial skin; A-T; 5s.

Tue Mar 27 09:32:17 2001

us-09-410-835-4.o119.rmg

Page 323

CC development in the bulbar conjunctiva and facial skin, and is later
 CC accompanied by graying of the hair and atrophied telangiectases in the conjunctiva
 CC co-occurrence of cerebellar ataxia and telangiectases in the conjunctiva
 CC and occasionally on the facial skin (the second early hallmark of A-T)
 CC cerebellar ataxia. The present sequence encodes a defective gene that causes A-T. The gene can also be used
 CC to generate antibodies. The antibodies and methods can be used in the
 CC study, diagnosis and therapy of A-T.
 XX
 SD Sequence 1254 BP: 417 A; 199 C; 220 G; 418 T; 0 other:
 Query Match 0.3%; Score 18; DB 19; Length 1254;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 385 atgagagagagagagagagag 402
 Db 66 atgagagagagagagagagag 49
 RESULT 193
 T43551/C
 ID T43551 standard: CDNA: 1265 BP.
 AC T43552;
 XX
 XX 08-DEC-1999 (first entry)
 DE Human breast tumour-associated EST 51.
 XX
 XX Expressed sequence tag; EST; human; breast; cancer; cytochrome;
 XX medicaments; gene therapy; treatment; 18S ribosomal; ss.
 XX
 XX Homo sapiens.
 XX
 XX DE19013035-A1.
 XX
 XX 20-MAR-1998; 98DE-1013035.
 XX
 XX 20-MAR-1998; 98DE-1013035.
 XX (HETA-1) HETAGS GDS GEMOROSCHING MDH.
 XX
 XX Spect T, Hinmann B, Schmitt A, Piletsky C, Dahl E, Rosenthal A;
 XX WPI: 1999-528979/45.
 XX

Tue Mar 27 09:32:17 2001

us-09-410-835-4.o119.rmg

Page 322

XX Homo sapiens.
 XX Key
 XX Intron
 XX
 XX Location/Qualifiers
 XX 1..103
 XX /tag= a
 XX /number= 47
 XX /tag= b
 XX 104..138
 XX /tag= d
 XX /number= 48
 XX 139..858
 XX /tag= c
 XX /number= 48
 XX 859..1026
 XX /tag= d
 XX /number= 49
 XX 1027..1254
 XX /tag= e
 XX /number= 49
 XX W09616691-A1.
 XX
 XX 21-NOV-1996.
 XX
 XX 16-MAY-1996; 96MO-0507025.
 XX
 XX 08-APR-1996; 96US-0639001.
 XX 16-MAY-1995; 95US-0441822.
 XX
 XX (KONN) KONN R I.
 XX (ORIN) UNIV RANOT APPLIED RES & IND DEV LTD.
 XX Shloh Y;
 XX WPI: 1997-012070/01.
 XX
 XX New isolated ataxia-telangiectasia gene - used to develop prods. for
 XX the study, diagnosis and treatment of ataxia-telangiectasia.
 XX
 XX Claim 1: Page 69: 133pp: English.
 XX
 XX T4344-T4346 represent exons of the ATM gene of the invention.
 XX Ataxia-telangiectasia (A-T) is caused by mutations, insertions, or
 XX deletions in the coding region of the ATM gene. A-T is a progressive
 XX genetic disorder affecting the central nervous and immune systems. A-T
 XX involves abnormalities in cell cycle regulation, DNA repair, and cell cycle abnormalities. A-T is a multi-system disease
 XX inherited in an autosomal recessive manner. Cerebellar ataxia that
 XX gradually develops into general motor dysfunction is the first clinical
 XX sign of A-T. The present sequence encodes a defective gene that causes
 XX the cerebellum, oculocutaneous telangiectasia (dilation of blood vessels)

Tue Mar 27 09:32:17 2001

us-09-410-835-4.o119.rmg

Page 324

XX Human nucleic acid sequences and protein products from normal breast
 XX tissue, useful for breast cancer therapy
 XX
 XX Claim 3: 139; 206pp: German.
 XX
 XX This invention describes novel human nucleic acid sequences from normal
 XX breast tissue which have cytostatic activity. The nucleic acid sequences
 XX can be used to express proteins, which can be used as cytostatic agents
 XX actively against breast cancer. The sequences can be used in sense or
 XX antisense form. They are especially useful for medicaments for gene
 XX therapy to treat breast cancer and for treating illnesses associated
 XX with breast cancer. The present sequence is a cDNA sequence expressed sequence tags
 XX described in the method of the invention.
 XX
 SD Sequence 1265 BP: 369 A; 252 C; 245 G; 399 T; 0 other:
 Query Match 0.3%; Score 18; DB 20; Length 1265;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 385 atgagagagagagagagagag 402
 Db 1245 atgagagagagagagagagag 1262
 RESULT 194
 O15023
 ID O15023 standard: CDNA: 1290 BP.
 AC O15023;
 XX
 XX 16-MAR-1992 (first entry)
 DE Rat prolactin coding sequence.
 XX
 XX rPR: plasmid pPR11; ds.
 XX
 XX Rattus.
 XX
 XX Key
 XX CDS
 XX polyA_signal
 XX /tag= b
 XX JF01347284-A.
 XX
 XX 05-NOV-1991.
 XX
 XX Location/Qualifiers
 XX 441..1121
 XX /tag= a
 XX 1122..1342
 XX /tag= b

Tue Mar 27 09:32:17 2001

us-09-410-035-4.01ig.rmg

Page 331

Tue Mar 27 09:32:17 2001

us-09-410-835-4.011g.rdg

Page 332

CC They may also be used as food additives or preservatives. A26772 to
CC A26280 and 191345 are sequences used in the exemplification of the
CC present invention.
XX
SQ Sequence 1350 BP: 458 A; 205 C; 196 G; 491 T; 0 other:

Query Match 0.3% Score 18: DB 19: Length 1358;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 816 CACCAAGGCACTCTCAT 833
 DB 133 CACCAAGGCACTCTCAT 156

RESULT 200
 V38742/c
 ID V38742 standard: cDNA: 1358 BP.
 AC V38742;
 XX 18-SEP-1998 (first entry)
 DT
 XX Complementary strand of cDNA nISPI2-1358 encoding a SPI protein.
 XX Serine protease inhibitor: SPI: anti-hematophagous ectoparasite:
 KW vaccine; control: flea; acarina; immune response: aa.
 XX Ctenocephalides felis.
 XX M09820034-A2.
 XX 14-MAY-1998.
 XX 05-NOV-1997; 97MO-US20678.
 PF 07-NOV-1996; 96US-0745995.
 PA (HEER-) HESKA CORP.
 XX Brandt KS, Maddux JD, Silver GH, Wisniewski N;
 DX WPI. 1998-28684/25.
 XX
 PT New nucleic acid encoding new serine protease inhibitors from fleas
 - and related antipodites, inhibitors, recombinant viruses and cells,
 useful for control of fleas on animals, especially cats and dogs
 XX Claim 2: Pages 104-105, 176pp: English.
 PS
 XX The present sequence represents the complementary strand of nISPI2-1358,
 CC which encodes a ctenocephalides felis serine protease inhibitor (SPI)
 CC and is a complementary strand of the complementary strand of the SPI
 CC anti-hematophagous ectoparasitic vaccine and drug compositions
 CC containing the inhibitor are used to control fleas (adults or larvae) on
 CC mammals or birds, particularly cats and dogs. More generally the

CC composition is also used for control of insects and acarina, on animals
 CC or on stored goods, plants, trees etc. including domestic pests and
 CC on stored goods, plants, trees etc. including domestic pests and
 CC a protective immune response against SPI.
 XX Sequence 1358 BP: 411 A: 263 C: 248 G: 436 T: 0 other;
 SO

Query Match 0.3% Score 18: DB 19: Length 1358;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 816 CACCAAGGCACTCTCAT 833
 DB 1220 CACCAAGGCACTCTCAT 1203

Search completed: March 26, 2001, 22:47:15
 Job time: 28931 sec

Copyright (c) 1993 - 2000 CompuGen Ltd.

OH nucleic - nucleic search, using sv model

Run on: March 26, 2001, 12:15:51 : Search time 6804.77 Seconds

(Without alignments)
6101,509 Million cell updates/sec

Title: US-09-410-835-4

Perfect score: 5925

Sequence: 1 cctccattttagactcca.....cttttagatagacaaagctt 5925

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 7991742 seqs, 350374858 residues

Word size: 15

Total number of hits satisfying chosen parameters: 272463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database: ESR:

1: gb.est1.*
2: gb.est2.*
3: gb.est3.*
4: gb.est4.*
5: gb.est5.*
6: gb.est6.*
7: gb.est7.*
8: gb.est8.*
9: gb.est9.*
10: gb.est10.*
11: gb.est11.*
12: gb.est12.*
13: gb.est13.*
14: gb.est14.*
15: gb.est15.*
16: gb.est16.*
17: gb.est17.*
18: gb.est18.*
19: gb.est19.*
20: gb.est20.*
21: gb.est21.*

73: em.est15.*
74: em.est16.*
75: em.est17.*
76: em.est18.*
77: em.est19.*
78: em.est20.*
79: em.est21.*
80: em.est22.*
81: em.est23.*
82: em.est24.*
83: em.est25.*
84: em.est26.*
85: em.est27.*
86: em.est28.*
87: em.est29.*
88: gb.est1.*
89: gb.est2.*
90: gb.est3.*
91: gb.est4.*
92: gb.est5.*
93: gb.est6.*
94: gb.est7.*
95: gb.est8.*
96: gb.est9.*
97: gb.est10.*
98: gb.est11.*
99: gb.est12.*
100: gb.est13.*
101: gb.est14.*
102: gb.est15.*
103: gb.est16.*
104: gb.est17.*
105: gb.est18.*
106: gb.est19.*
107: gb.est20.*
108: gb.est21.*
109: gb.est22.*
110: gb.est23.*
111: gb.est24.*
112: gb.est25.*
113: em.esthum1.*
114: em.esthum2.*
115: em.esthum3.*
116: em.esthum4.*
117: em.esthum5.*
118: em.esthum6.*
119: em.esthum7.*
120: em.esthum8.*
121: em.esthum9.*
122: em.esthum10.*
123: em.esthum11.*

22: gb.est22.*
23: gb.est23.*
24: gb.est24.*
25: gb.est25.*
26: gb.est26.*
27: gb.est27.*
28: gb.est28.*
29: gb.est29.*
30: gb.est30.*
31: gb.est31.*
32: gb.est32.*
33: gb.est33.*
34: gb.est34.*
35: gb.est35.*
36: gb.est36.*
37: gb.est37.*
38: gb.est38.*
39: gb.est39.*
40: gb.est40.*
41: em.est1.*
42: em.est2.*
43: em.est3.*
44: em.est4.*
45: em.est5.*
46: em.est6.*
47: em.est7.*
48: em.est8.*
49: em.est9.*
50: em.est10.*
51: em.est11.*
52: em.est12.*
53: em.est13.*
54: em.est14.*
55: em.est15.*
56: em.est16.*
57: em.est17.*
58: em.est18.*
59: em.est19.*
60: em.est20.*
61: em.est21.*
62: em.est22.*
63: em.est23.*
64: em.est24.*
65: em.est25.*
66: em.est26.*
67: em.est27.*
68: em.est28.*
69: em.est29.*
70: em.est30.*
71: em.est31.*
72: em.est32.*

124: em.est18.*
125: em.est19.*
126: em.est20.*
127: gb.est1.*
128: gb.est2.*
129: gb.est3.*
130: gb.est4.*
131: gb.est5.*
132: gb.est6.*
133: gb.est7.*
134: gb.est8.*
135: gb.est9.*
136: gb.est10.*
137: gb.est11.*
138: gb.est12.*
139: gb.est13.*
140: gb.est14.*
141: gb.est15.*
142: gb.est16.*
143: gb.est17.*
144: gb.est18.*
145: gb.est19.*
146: gb.est20.*
147: gb.est21.*
148: gb.est22.*
149: gb.est23.*
150: gb.est24.*
151: gb.est25.*
152: em.est1.*
153: em.est2.*
154: em.est3.*
155: em.est4.*
156: gb.est1.*
157: gb.est2.*
158: gb.est3.*
159: em.est1.*
160: gb.est1.*
161: gb.est2.*
162: gb.est3.*
163: em.est1.*
164: em.est2.*
165: gb.est1.*
166: gb.est2.*
167: em.est1.*
168: em.est2.*
169: em.est3.*
170: em.est4.*
171: gb.est1.*
172: gb.est2.*
173: gb.est3.*
174: gb.est4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	DB	ID	Description
1	175	0.4	621	110	BE577445	BE577445 L48-2287T
2	176	0.4	646	110	BE577469	BE577469 L48-2215T
3	177	0.4	260	111	BM444908	BM444908 BM444908
4	178	0.4	260	111	BM444908	BM444908 BM444908
5	179	0.4	294	112	BM445792	BM445792 BM445792
6	180	0.4	411	221	AI591454	AI591454 vus1402.x
7	181	0.4	416	105	BE217300	BE217300 146442.NA
8	182	0.4	589	136	BE821724	BE821724 uc26010.x
9	183	0.4	539	36	AV365015	AV365015 AV365015
10	184	0.4	592	180	A2384548	A2384548 1M0142C11
11	185	0.4	1026	138	BE963593	BE963593 1601657194
12	186	0.4	150	157	AL084411	AL084411 M6C524025
13	187	0.4	127	115	AI054251	AI054251 4372011.x
14	188	0.4	176	29	A0092452	A0092452 A0092452
15	189	0.4	185	25	AI816709	AI816709 UT-M-A0-
16	190	0.4	230	25	AI815982	AI815982 UT-M-A00
17	191	0.4	233	115	BE518829	BE518829 204054.NA
18	192	0.4	237	134	AV390224	AV390224 AV390224
19	193	0.4	247	190	CNS0005F	AL085317 Arabidops

74	21	0.4	492	28	AT002267	AT002267 AT002267
75	21	0.4	497	28	AL174022	AL174022 M6B04501
76	21	0.4	500	28	BE809028	BE809028 214167.NA
77	21	0.4	509	116	BE809028	BE809028 M6C524025
78	21	0.4	511	120	AL058124	AL058124 M6C524025
79	21	0.4	519	29	A0096044	A0096044 A0096044
80	21	0.4	522	12	AA832599	AA832599 vus1402.x
81	21	0.4	531	134	BE031628	BE031628 M6C524025
82	21	0.4	542	39	AM028928	AM028928 M6C524025
83	21	0.4	546	25	AL783160	AL783160 B58M13821
84	21	0.4	551	37	AV549932	AV549932 AV549932
85	21	0.4	574	164	B654765	B654765 T1229R.TM
86	21	0.4	574	164	B654765	B654765 T1229R.TM
87	21	0.4	598	177	AZ235445	AZ235445 RCT1-31-7
88	21	0.4	606	36	AV386003	AV386003 AV386003
89	21	0.4	614	38	AV699504	AV699504 AV699504
90	21	0.4	620	132	AB8501MHP	AB8501MHP 1601657194
91	21	0.4	670	160	AO491444	AO491444 RCT1-11-2
92	21	0.4	692	180	A2382945	A2382945 1M0142C11
93	21	0.4	712	139	AO110183	AO110183 C17-HSP-2
94	21	0.4	742	191	CNS00457	CNS00457 M6C524025
95	21	0.4	757	176	A2195068	A2195068 SP-1029.A
96	21	0.4	781	106	BE269463	BE269463 001184638
97	21	0.4	921	151	AE642829	AE642829 M6B04501
98	21	0.4	951	151	AE642829	AE642829 M6B04501
99	21	0.4	951	151	AE642829	AE642829 M6B04501
100	21	0.4	951	151	AE642829	AE642829 M6B04501
101	21	0.4	951	151	AE642829	AE642829 M6B04501
102	21	0.4	951	151	AE642829	AE642829 M6B04501
103	21	0.4	951	151	AE642829	AE642829 M6B04501
104	21	0.4	951	151	AE642829	AE642829 M6B04501
105	21	0.4	951	151	AE642829	AE642829 M6B04501
106	21	0.4	951	151	AE642829	AE642829 M6B04501
107	21	0.4	951	151	AE642829	AE642829 M6B04501
108	21	0.4	951	151	AE642829	AE642829 M6B04501
109	21	0.4	951	151	AE642829	AE642829 M6B04501
110	21	0.4	951	151	AE642829	AE642829 M6B04501
111	21	0.4	951	151	AE642829	AE642829 M6B04501
112	21	0.4	951	151	AE642829	AE642829 M6B04501
113	21	0.4	951	151	AE642829	AE642829 M6B04501
114	21	0.4	951	151	AE642829	AE642829 M6B04501
115	21	0.4	951	151	AE642829	AE642829 M6B04501
116	21	0.4	951	151	AE642829	AE642829 M6B04501
117	21	0.4	951	151	AE642829	AE642829 M6B04501
118	21	0.4	951	151	AE642829	AE642829 M6B04501
119	21	0.4	951	151	AE642829	AE642829 M6B04501
120	21	0.4	951	151	AE642829	AE642829 M6B04501
121	21	0.4	951	151	AE642829	AE642829 M6B04501
122	21	0.4	951	151	AE642829	AE642829 M6B04501
123	21	0.4	951	151	AE642829	AE642829 M6B04501
124	21	0.4	951	151	AE642829	AE642829 M6B04501

c 176 305 144 R46662
 c 177 305 150 AQ21022
 c 178 306 150 B555459
 c 179 306 150 B555459
 c 180 310 138 BR02135
 c 181 311 138 BR02135
 c 182 312 15 A1073068
 c 183 312 15 A1073068
 c 184 312 15 A1073068
 c 185 315 88 A265414
 c 186 315 126 B276510
 c 187 318 23 A1687836
 c 188 318 23 B276510
 c 189 319 24 A1751085
 c 190 319 24 A1751085
 c 191 324 93 A067887
 c 192 324 93 A067887
 c 193 324 93 A067887
 c 194 324 93 A067887
 c 195 324 93 A067887
 c 196 324 93 A067887
 c 197 324 93 A067887
 c 198 324 93 A067887
 c 199 324 93 A067887
 c 200 330 141 H4282
 c 201 330 141 H4282
 c 202 330 141 H4282
 c 203 330 141 H4282
 c 204 330 141 H4282
 c 205 330 141 H4282
 c 206 330 141 H4282
 c 207 330 141 H4282
 c 208 330 141 H4282
 c 209 330 141 H4282
 c 210 330 141 H4282
 c 211 330 141 H4282
 c 212 330 141 H4282
 c 213 330 141 H4282
 c 214 330 141 H4282
 c 215 330 141 H4282
 c 216 330 141 H4282
 c 217 330 141 H4282
 c 218 330 141 H4282
 c 219 330 141 H4282
 c 220 330 141 H4282
 c 221 330 141 H4282
 c 222 330 141 H4282
 c 223 330 141 H4282
 c 224 330 141 H4282
 c 225 330 141 H4282
 c 226 330 141 H4282

c 227 355 88 A093471
 c 228 357 89 A093471
 c 229 357 89 A093471
 c 230 357 89 A093471
 c 231 357 89 A093471
 c 232 357 89 A093471
 c 233 357 89 A093471
 c 234 357 89 A093471
 c 235 357 89 A093471
 c 236 357 89 A093471
 c 237 357 89 A093471
 c 238 357 89 A093471
 c 239 357 89 A093471
 c 240 357 89 A093471
 c 241 357 89 A093471
 c 242 357 89 A093471
 c 243 357 89 A093471
 c 244 357 89 A093471
 c 245 357 89 A093471
 c 246 357 89 A093471
 c 247 357 89 A093471
 c 248 357 89 A093471
 c 249 357 89 A093471
 c 250 357 89 A093471
 c 251 357 89 A093471
 c 252 357 89 A093471
 c 253 357 89 A093471
 c 254 357 89 A093471
 c 255 357 89 A093471
 c 256 357 89 A093471
 c 257 357 89 A093471
 c 258 357 89 A093471
 c 259 357 89 A093471
 c 260 357 89 A093471
 c 261 357 89 A093471
 c 262 357 89 A093471
 c 263 357 89 A093471
 c 264 357 89 A093471
 c 265 357 89 A093471
 c 266 357 89 A093471
 c 267 357 89 A093471
 c 268 357 89 A093471
 c 269 357 89 A093471
 c 270 357 89 A093471
 c 271 357 89 A093471
 c 272 357 89 A093471
 c 273 357 89 A093471
 c 274 357 89 A093471
 c 275 357 89 A093471
 c 276 357 89 A093471
 c 277 357 89 A093471

c 278 411 89 A093471
 c 279 411 89 A093471
 c 280 411 89 A093471
 c 281 411 89 A093471
 c 282 411 89 A093471
 c 283 411 89 A093471
 c 284 411 89 A093471
 c 285 411 89 A093471
 c 286 411 89 A093471
 c 287 411 89 A093471
 c 288 411 89 A093471
 c 289 411 89 A093471
 c 290 411 89 A093471
 c 291 411 89 A093471
 c 292 411 89 A093471
 c 293 411 89 A093471
 c 294 411 89 A093471
 c 295 411 89 A093471
 c 296 411 89 A093471
 c 297 411 89 A093471
 c 298 411 89 A093471
 c 299 411 89 A093471
 c 300 411 89 A093471
 c 301 411 89 A093471
 c 302 411 89 A093471
 c 303 411 89 A093471
 c 304 411 89 A093471
 c 305 411 89 A093471
 c 306 411 89 A093471
 c 307 411 89 A093471
 c 308 411 89 A093471
 c 309 411 89 A093471
 c 310 411 89 A093471
 c 311 411 89 A093471
 c 312 411 89 A093471
 c 313 411 89 A093471
 c 314 411 89 A093471
 c 315 411 89 A093471
 c 316 411 89 A093471
 c 317 411 89 A093471
 c 318 411 89 A093471
 c 319 411 89 A093471
 c 320 411 89 A093471
 c 321 411 89 A093471
 c 322 411 89 A093471
 c 323 411 89 A093471
 c 324 411 89 A093471
 c 325 411 89 A093471
 c 326 411 89 A093471
 c 327 411 89 A093471
 c 328 411 89 A093471

c 329 456 40 A093471
 c 330 456 40 A093471
 c 331 456 40 A093471
 c 332 456 40 A093471
 c 333 456 40 A093471
 c 334 456 40 A093471
 c 335 456 40 A093471
 c 336 456 40 A093471
 c 337 456 40 A093471
 c 338 456 40 A093471
 c 339 456 40 A093471
 c 340 456 40 A093471
 c 341 456 40 A093471
 c 342 456 40 A093471
 c 343 456 40 A093471
 c 344 456 40 A093471
 c 345 456 40 A093471
 c 346 456 40 A093471
 c 347 456 40 A093471
 c 348 456 40 A093471
 c 349 456 40 A093471
 c 350 456 40 A093471
 c 351 456 40 A093471
 c 352 456 40 A093471
 c 353 456 40 A093471
 c 354 456 40 A093471
 c 355 456 40 A093471
 c 356 456 40 A093471
 c 357 456 40 A093471
 c 358 456 40 A093471
 c 359 456 40 A093471
 c 360 456 40 A093471
 c 361 456 40 A093471
 c 362 456 40 A093471
 c 363 456 40 A093471
 c 364 456 40 A093471
 c 365 456 40 A093471
 c 366 456 40 A093471
 c 367 456 40 A093471
 c 368 456 40 A093471
 c 369 456 40 A093471
 c 370 456 40 A093471
 c 371 456 40 A093471
 c 372 456 40 A093471
 c 373 456 40 A093471
 c 374 456 40 A093471
 c 375 456 40 A093471
 c 376 456 40 A093471
 c 377 456 40 A093471
 c 378 456 40 A093471
 c 379 456 40 A093471

RESULT 3
 BE577445/c 621 bp mRNA EST
 LOCUS L48-22873 Ice plant Lambda Uni-Tap XR expression library, 48 hours
 DEFINITION NCI treatment Mesembryanthemum crystallinum cDNA clone L48-2287
 BE577445 sequence.
 BE577445 1 GI:987244
 KEYWORDS
 SOURCE common ice plant, crystallinum
 ORGANISM Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllaceae; Mesembryanthemum.
 REFERENCE 1. bases 1 to 621
 JOURNAL An expressed sequence tag database for the common ice plant.
 COMMENT Unpublished (1997)
 CONTACT: Chuanman JC
 DEPARTMENT: Department of Biochemistry and Molecular Biology
 350 Noble Research Center, Stillwater, OK 74078-3035, USA
 Tel.: 405-744-6207
 Fax: 405-744-7799
 Email: jchuanman@biochem.okstate.edu
 PCR PRIMER: 73
 FORWARD: 73
 REVERSE: 73
 Seq primer: 73
 High quality sequence stop: 350
 POLYA-No.

ALIGNMENTS

Query Match 0.41; Score 23; DB 110; Length 646;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 380 TGAATGATGAAAAAAGAAAAA 402
 25 TCAATTAATCAAAAAAAGAAAAA 3

Tue Mar 27 09:32:21 2001

us-09-410-835-4.0119.txt

Page 27

FEATURES
 source HIGH quality sequence stop: 350
 POLYA-No. Location/Qualifiers
 1. 646
 /organism="Mesembryanthemum crystallinum"
 /db_xref="taxon:3544"
 /clone_lib="Ice plant Lambda Uni-Tap XR expression library"
 /clone_lib="Ice plant Lambda Uni-Tap XR expression library"
 /tissue_type="Leaf", 48 h 0.4M NaCl*
 /tissue_type="Leaf", 48 h 0.4M NaCl*
 /note="Stage-Six week old Uni-Tap XR, Blue-script SK-; Site-1;
 EcorI; Site-2; XhoI"
 BASE COUNT 175 a 119 c 137 g 215 t
 ORIGIN

Query Match 0.41; Score 23; DB 110; Length 646;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 380 TGAATGATGAAAAAAGAAAAA 402
 25 TCAATTAATCAAAAAAAGAAAAA 3

RESULT 3
 BE464908 260 bp mRNA EST
 LOCUS BE464908 RIKEN full-length cDNA clone D13095H16.3, mRNA sequence.
 DEFINITION Mus musculus cDNA clone D13095H16.3, mRNA sequence.
 BE464908 1 GI:9382097
 KEYWORDS
 SOURCE House mouse
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1. bases 1 to 260
 JOURNAL Unpublished (2000)
 CONTACT: Kiyoshi H. et al.
 DEPARTMENT: Genome Exploration Research Group, Life Science Research Center,
 Genome Science Laboratory
 The Institute of Physical and Chemical Research (RIKEN), Genomic
 Sciences Center, Tsukuba, Ibaraki 305-0074, Japan
 Tel.: +81-298-36-9098
 Fax: +81-298-36-9098
 Email: kiyoshi@riken.go.jp
 PCR PRIMER: 73
 FORWARD: 73
 REVERSE: 73
 Seq primer: 73
 High quality sequence stop: 350
 POLYA-No.

Tue Mar 27 09:32:21 2001

us-09-410-835-4.0119.txt

Page 26

Query Match 0.41; Score 23; DB 110; Length 621;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 380 TGAATGATGAAAAAAGAAAAA 402
 25 TCAATTAATCAAAAAAAGAAAAA 3

RESULT 3
 BE577445/c 646 bp mRNA EST
 LOCUS L48-22873 Ice plant Lambda Uni-Tap XR expression library, 48 hours
 DEFINITION NCI treatment Mesembryanthemum crystallinum cDNA clone L48-2287
 BE577445 sequence.
 BE577445 1 GI:987244
 KEYWORDS
 SOURCE common ice plant, crystallinum
 ORGANISM Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllaceae; Mesembryanthemum.
 REFERENCE 1. bases 1 to 646
 JOURNAL An expressed sequence tag database for the common ice plant.
 COMMENT Unpublished (1997)
 CONTACT: Chuanman JC
 DEPARTMENT: Department of Biochemistry and Molecular Biology
 350 Noble Research Center, Stillwater, OK 74078-3035, USA
 Tel.: 405-744-6207
 Fax: 405-744-7799
 Email: jchuanman@biochem.okstate.edu
 PCR PRIMER: 73
 FORWARD: 73
 REVERSE: 73
 Seq primer: 73
 High quality sequence stop: 350
 POLYA-No.

Tue Mar 27 09:32:21 2001

us-09-410-835-4.0119.txt

Page 28

FEATURES
 source RIKEN Mouse ESTs (Kondo, H., et al.)
 JOURNAL Unpublished (2000) Hayashizaki
 COMMENT Genome Exploration Research Group, Life Science Research Center,
 Genome Science Laboratory
 The Institute of Physical and Chemical Research (RIKEN), Genomic
 Sciences Center, Tsukuba, Ibaraki 305-0074, Japan
 Tel.: +81-298-36-9098
 Fax: +81-298-36-9098
 Email: kiyoshi@riken.go.jp
 PCR PRIMER: 73
 FORWARD: 73
 REVERSE: 73
 Seq primer: 73
 High quality sequence stop: 350
 POLYA-No.

Query Match 0.41; Score 23; DB 110; Length 621;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 380 TGAATGATGAAAAAAGAAAAA 402
 25 TCAATTAATCAAAAAAAGAAAAA 3

BASE COUNT 66 a 92 c 43 g 87 t
ORIGIN

Query Match 0.43; Score 22; DB 131; Length 260;
Best Local Similarity 100.0%; Pred No. 23;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 2502 ggcgcgaactgaactgaact 2603
180 TCTCTCAATCACTCAATCACT 159

RESULT 4
LOCUS B845782 277 bp mRNA EST 23-JUL-2000
DEFINITION B845782 RIKEN full-length enriched, 13 days embryo lung Mus
ACCESSION B845782.1 GI:9403391
VERSION B845782.1 GI:9403391
KEYWORDS EST
SOURCE Mus musculus
ORGANISM Mus musculus
CHORDATA: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus:
1 (bases 1 to 277)
P. Endo, T. Fukuda, S. Fukunishi, Y. Iwata, A. Hayashi, N. Iizawa, M. Iwata, K. Kageyama, I. Kaji, C. Kawai, J. Kikuchi, M. Kiyosawa, H. Kojima, Y. Kondo, S. Koyama, S. Kunitake, C. Kusakabe, M. Matsuyama, T. Miki, K. Mizuno, Y. Nakamura, H. Oda, H. Ohtsuki, Y. Ono, T. Ooi, C. Sakai, C. Sato, K. Shibata, K. Shiba, Y. Suzuki, H. Suzuki, H. Tagawa, A. Takahashi, F. Tomioka, N. Toyama, T. Tsumoda, Y. Watanabe, S. Yamamura, T. Yamashita, I. Yano, R. Yasunishi, A. Yokota, T. Yoshida, K. Yoshida, A. Yoshino, H. Muramatsu, M. and Hayashizaki, Y.
Unpublished (2000)
Contact: Yoshinori Hayashizaki
Genome Exploration Research Group, Life Science Tsubuka Center,
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
3-1-1 Koyadai, Tsubuka, Ibaraki 305-0074, Japan
Tel.: +81-298-36-5013
Fax: +81-298-36-5020
Email: genome-research@riken.go.jp/
URL: http://genome.riken.go.jp/

TITLE
JOURNAL
COMMENT

Genome Exploration Research Group, Life Science Tsubuka Center,
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
3-1-1 Koyadai, Tsubuka, Ibaraki 305-0074, Japan
Tel.: +81-298-36-5013
Fax: +81-298-36-5020
Email: genome-research@riken.go.jp/
URL: http://genome.riken.go.jp/

RESULT 5
LOCUS B845792 294 bp mRNA EST 26-JUL-2000
DEFINITION B845792 RIKEN full-length enriched, 13 days embryo stomach Mus
ACCESSION B845792.1 GI:9467975
VERSION B845792.1 GI:9467975
KEYWORDS EST
SOURCE Mus musculus
ORGANISM Mus musculus
CHORDATA: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus:
1 (bases 1 to 294)
P. Endo, T. Fukuda, S. Fukunishi, Y. Iwata, A. Hayashi, N. Iizawa, M. Iwata, K. Kageyama, I. Kaji, C. Kawai, J. Kikuchi, M. Kiyosawa, H. Kojima, Y. Kondo, S. Koyama, S. Kunitake, C. Kusakabe, M. Matsuyama, T. Miki, K. Mizuno, Y. Nakamura, H. Oda, H. Ohtsuki, Y. Ono, T. Ooi, C. Sakai, C. Sato, K. Shibata, K. Shiba, Y. Suzuki, H. Suzuki, H. Tagawa, A. Takahashi, F. Tomioka, N. Toyama, T. Tsumoda, Y. Watanabe, S. Yamamura, T. Yamashita, I. Yano, R. Yasunishi, A. Yokota, T. Yoshida, K. Yoshida, A. Yoshino, H. Muramatsu, M. and Hayashizaki, Y.
Unpublished (2000)
Contact: Yoshinori Hayashizaki
Genome Exploration Research Group, Life Science Tsubuka Center,
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
3-1-1 Koyadai, Tsubuka, Ibaraki 305-0074, Japan
Tel.: +81-298-36-5013
Fax: +81-298-36-5020
Email: genome-research@riken.go.jp/
URL: http://genome.riken.go.jp/

TITLE
JOURNAL
COMMENT

Genome Exploration Research Group, Life Science Tsubuka Center,
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
3-1-1 Koyadai, Tsubuka, Ibaraki 305-0074, Japan
Tel.: +81-298-36-5013
Fax: +81-298-36-5020
Email: genome-research@riken.go.jp/
URL: http://genome.riken.go.jp/

Carninci, P., Nishiyama, Y., Nease, A., Itoh, M., Nagao, S., Sasaki, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tomioka, N., Toyama, T., Tsumoda, Y., Watanabe, S., Yamamura, T., Yamashita, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshida, A., Yoshino, H. Muramatsu, M. and Hayashizaki, Y.
Unpublished (2000)
Contact: Yoshinori Hayashizaki
Genome Exploration Research Group, Life Science Tsubuka Center,
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
3-1-1 Koyadai, Tsubuka, Ibaraki 305-0074, Japan
Tel.: +81-298-36-5013
Fax: +81-298-36-5020
Email: genome-research@riken.go.jp/
URL: http://genome.riken.go.jp/

BASE COUNT 65 a 92 c 43 g 87 t
ORIGIN

Query Match 0.43; Score 22; DB 131; Length 277;
Best Local Similarity 100.0%; Pred No. 23;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 330 ggcgcgaactgaactgaact 403
62 CATCTCAATCACTCAATCACT 41

RESULT 6
LOCUS A159344 411 bp mRNA EST 23-JUL-1999
DEFINITION A159344 3' SmaI site, human HEPARIN-BINDING GROWTH FACTOR
ACCESSION A159344.1 GI:4602542
VERSION A159344.1 GI:4602542
KEYWORDS EST
SOURCE house mouse.

BASE COUNT 65 a 92 c 43 g 87 t
ORIGIN

Query Match 0.44; Score 22; DB 132; Length 294;
Best Local Similarity 100.0%; Pred No. 23;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 215 ggcgcgaactgaactgaact 2603
215 TCTCTCAATCACTCAATCACT 194

Tue Mar 27 09:32:21 2001

us-09-410-835-4.01ig.rst

Page 39

Tue Mar 27 09:32:21 200

us-09-410-835-4.01lg.rst

Page 40

Tue Mar 27 09:32:21 200

us-09-410-835-4.011g.rst

Page 40

RESULT	15
AI054251/c	
LOCUS	172 bp mRNA
DEFINITION	g1172111.11 NCL-CONP-Ov6 Homo sapiens cDNA clone IMAGE:185433 , mRNA sequence.

ACCESSION	AI054251
VERSION	AI054251.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
EuArchaea: Metazoa: Chordata: Vertebrata: Euteleostomi:	

Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

```

Query Match      0: 48: Score 21: DB 15: Length 172:
Best Local Similarity 100.0%: Pred. No. 77:
Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 302 attaaatgaaaaaaaaaaaaa 402
|||||
|||
7 ATTAAATGAAAAAAAAAAAAA 7
Db

```

AUTHORS	Sasaki, T. and Yamamoto, K.
TITLE	Rice cDNA from callus (2000)
JOURNAL	Unpublished (2000)
COMMENT	Contact: Takuji Sasaki


```

/db_xref="taxon:109090"
/clone="U1-M-A00-ab-6-10-0-UI"
/clone_lib="NH-BMAP-NMT"
/lab_host="MD108 (Life Technologies)"
/linker="vector: p717D-Pac (Pharmacia)"
/polylinker_site:1: Not I; Site:2: Eco RI; The
NH-BMAP-NMT library is a non-normalized library
of cDNA fragments prepared by ligating the
ends of 5 nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lemon and Soares, Genome Research 6: 791-800
(1996).
Lytic Miller Laboratories
Lytic-Miller-BMAP-NMT
TAC LIB=NH-BMAP-NMT
TAC TISSUE=hippocampus
TAC_SEQ=TCGA 36 g 61 t
76 a 37 c

```

Tue Mar 27 09:32:21 2001

us-09-410-835-4.011g.rst

Page 51

Tue Mar 27 09:32:21 2001

us-09-410-835-4.0119.txt

Page 52

```

atralin="CS7BL/6J"
/db_xref="taxon:10930"
/clone="J1330003"
/notes="Riken full-length enriched, 10 days neonate
intestinal"
/sex="Mixed"
/tissue="Intestine"
/ab_pos="5'-noncoding region"
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken

```

CONCLUSION
REFERENCES
Bakkerius, W. J. L. 1993. *Phylogeny, Biogeography, Tracheophyta, Euphyllophytes, Spermatophytes, Magnoliopsida, endicots, core eudicots, Rosidae, eurosid II, Brassicales, Brassicaceae, Arabidopsis*. (247)
Samson, D., Saurin, N., Chomne, N., Attiguenne, F., Grotier, P., and Queller, P. 1999. *Unpublished*. (1 to 247)
JOURNAL
R. AUTHOR'S
TITLE
JOURNAL
Submitted (25-JUN-1999) Genoscope - Centre National de Séquençage

BP 191 91006 EYR cedex - FRANCE (E-mail: seqrefgenoscope.cnrs.fr)
 Web: www.genoscope.cns.fr
 FAXES: 33-1-42777777
 Source: /organism="Rattus norvegicus"
 /strain="Colimbia"
 /clone="10116"
 /dev_stage="adult"

Query Match 0.48; Score 21; DB 190; Length 247;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1800 aactgagatgaagatccca 1820
 DB 140 ACTGATGATGATTCCTCA 120

RESULT 23
 AAG97094 254 bp mRNA EST 04-JUN-1999
 DEFINITION UI-R-CO-hr-c-03-0-UI-R-CO Rattus norvegicus cDNA clone
 UI-R-CO-hr-c-03-0-UI-R-CO mRNA sequence.
 ACCESSION AAG97094
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Rattus; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 Genom Res. 6 (3), 791-806 (1996)
 JOURNAL 9704477
 MEDLINE
 COMMENT On Jun 5, 1998 this sequence version replaced gi:1187955.
 Contact: Soares, MB
 Department of Cell Discovery and Mapping
 University of Iowa
 431 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel.: 319 335 8250
 Fax: 319 335 8250
 Email: msoares@iastate.edu
 The sequence tag present in the cDNA between the NotI site and the

Qy 382 attatgaagaaagaaagaa 402
 DB 24 ATATATGATGATTCCTCA 4

RESULT 24
 A1707031 254 bp mRNA EST 03-JUN-1999
 LOCUS UI-R-ADI-m-e-07-0-UI-R-ADI Rattus norvegicus cDNA clone
 DEFINITION UI-R-ADI-m-e-07-0-UI-R-ADI mRNA sequence.
 ACCESSION A1707031
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Rattus; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 Genom Res. 6 (3), 791-806 (1996)
 JOURNAL 9704477
 MEDLINE
 COMMENT Contact: Soares, MB
 Department of Cell Discovery and Mapping
 University of Iowa
 431 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel.: 319 335 8250
 Fax: 319 335 8250
 Email: msoares@iastate.edu
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the poly A tail is a string of 5 nucleotides present
 between the NotI site and the oligo-dT track. The
 library was constructed as described by Bonaldo, Lennon
 and Soares (1996).
 Research Genetics (www.resgen.com) The following repetitive
 sequence is present in this cDNA sequence: 60-95.
 Seq primer: M3 Forward
 POLYA-yes.

FEATURES

Location/Qualifiers
 /organism="Rattus norvegicus"
 /strain="Spreague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-ADI-m-e-07-0-UI-R-ADI"
 /dev_stage="adult"

oligo-dT track served to identify it as a clone from the normalized
 adult ovary library. cDNA library preparation: M. Patricia Bonaldo,
 Department of Cell Discovery and Mapping, University of Iowa, Iowa
 City, IA 52242, USA. This clone is also available through the I.M.A.G.E.
 Consortium at LMB (InfoImage: lmb.gov). IMAGE ID:1781804 The
 following repetitive elements were found in this cDNA sequence:
 Seq primer: M3 Forward
 POLYA-yes

FEATURES
 Location/Qualifiers
 1..254
 /organism="Rattus norvegicus"
 /strain="Spreague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-CO-hr-c-03-0-UI-R-CO"
 /clone="10116"
 /dev_stage="adult"

Query Match 0.48; Score 21; DB 14; Length 254;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1800 aactgagatgaagatccca 1820
 DB 140 ACTGATGATGATTCCTCA 120

RESULT 23
 AAG97094 254 bp mRNA EST 04-JUN-1999
 DEFINITION UI-R-CO-hr-c-03-0-UI-R-CO Rattus norvegicus cDNA clone
 UI-R-CO-hr-c-03-0-UI-R-CO mRNA sequence.
 ACCESSION AAG97094
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Rattus; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 Genom Res. 6 (3), 791-806 (1996)
 JOURNAL 9704477
 MEDLINE
 COMMENT On Jun 5, 1998 this sequence version replaced gi:1187955.
 Contact: Soares, MB
 Department of Cell Discovery and Mapping
 University of Iowa
 431 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel.: 319 335 8250
 Fax: 319 335 8250
 Email: msoares@iastate.edu
 The sequence tag present in the cDNA between the NotI site and the

Qy 382 attatgaagaaagaaagaa 402
 DB 24 ATATATGATGATTCCTCA 4

RESULT 25
 A1047499 262 bp mRNA EST 01-MAR-2000
 LOCUS DNR255662121.S1586 (YHONMPC-hucl) Homo sapiens cDNA clone
 DEFINITION A1047499
 ACCESSION A1047499
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Klenzmann,B., Obermayer,B., Hesse,H.W., Gassenhuber,J. and
 EST (Ottensmeyer, et al.)
 JOURNAL 9704477
 MEDLINE
 COMMENT Contact: Ottensmeyer, B
 Department of Cell Discovery and Mapping
 University of Iowa
 431 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel.: 319 335 8250
 Fax: 319 335 8250
 Email: msoares@iastate.edu
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the poly A tail is a string of 5 nucleotides present
 between the NotI site and the oligo-dT track. The
 library was constructed as described by Bonaldo, Lennon
 and Soares (1996).
 Research Genetics (www.resgen.com) The following repetitive
 sequence is present in this cDNA sequence: 60-95.
 Seq primer: M3 Forward
 POLYA-yes.

FEATURES

Location/Qualifiers
 /organism="Rattus norvegicus"
 /strain="Spreague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-ADI-m-e-07-0-UI-R-ADI"
 /dev_stage="adult"

ACCESSION BE227191
 VERSION BE227191.1 GI:8932427
 KEYWORDS EST
 SOURCE House mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 380)
 NCICGP http://www.ncbi.nlm.nih.gov/ncicgp.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Human Gene Index
 JOURNAL Other-ESTs: w578405.x1
 COMMENT Contact: Robert Steinhilber, Ph.D.
 Tel: (301) 465-1550
 Fax: (301) 465-1550
 Email: steinhilber@nih.gov
 Tissue Procurement: Lohrer Hennighausen Ph.D., Priscilla Puth
 Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)
 Clone Distribution: NCICGP
 Clone through the I.M.A.G.E. Consortium/ILML at:
 Image.1101.gov/image/hnal/liferesources.shtml
 NC1:1066628

FEATURES

High quality sequence stop: 378.
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="NM1"
 /db_xref="taxon:10090"
 /clone="IMAGE:357284"
 /library="CDNA"
 /tissue_type="tumor, gross tissue"
 /dev_stage="5 months"
 /lab_host="DH10B"

BASE COUNT

132 a 0.4% Score 21: DB 105: Length 380:
 78 c 0.1%
 95 g 0.1%
 78 t 0.1%

Query Match 0.4% Score 21: DB 105: Length 380:
 Best Local Similarity 100.0% Pred. No. 71:
 Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Best Local Similarity 100.0% Pred. No. 71:
 Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Oy 382 attcaagaaagaaaaaa 402
 Db 29 ATTATCAAAAATAAAAAA 9
 RESULT 42
 ANS38569 301 bp mRNA EST 06-MAR-2000
 DEFINITION UT-8-B71-8ko-h-04-0-UI 3', mRNA sequence.
 ACCESSION ANS38569.1 GI:7170983
 VERSION ANS38569.1
 KEYWORDS Not a rat.
 SOURCE Rattus norvegicus
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 1 (bases 1 to 391)
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 CONTACT: Soares, MB
 Address: 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@iastate.edu
 The sequence was derived from a cDNA library that was present in the
 o11g database. The sequence was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo start tract is identical to the clone from the
 o11g database. The sequence tag between the NotI site and the
 source lab clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILML at:
 Image.1101.gov/image/hnal/liferesources.shtml
 Seq primer: M13 Forward

FEATURES

Location/Qualifiers
 1. 391
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /clone="UT-8-B71-8ko-h-04-0-UI"
 /clone_lib="UI-R-B71"

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Oy 2403 tttagagaaagatgagaga 2423
 Db 84 tttagagaaagatgagaga 104
 RESULT 43
 AL041690 387 bp mRNA EST 29-FEB-2000
 DEFINITION DREF2434N1917.s1 434 (synonym: h1c3) Homo sapiens cDNA clone
 DREF2434N1917.3', mRNA sequence.
 ACCESSION AL041690.1 GI:5421039
 VERSION AL041690.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 387)
 Bloeker, H., Boecker, H., Brandt, P., Hewes, H.W., Gassenhuber, J., and
 EST (Bloeker, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Bloeker, H.
 MFS
 MFS: Bloeker, H., Boecker, H., Brandt, P., Hewes, H.W., Gassenhuber, J., and
 This is the 3' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de,
 funded by the National Research Centre for Biotechnology Ltd.,
 German Genome Project. Within the cDNA sequencing consortium of the
 German Genome Project.
 No sequence available.
 This clone (DREF2434N1917) is available at the RGD in Berlin.
 Berlin-Charlottenburg, GERMANY. Email: clone@rgd.de
 Location/Qualifiers
 1. 387
 /organism="Homo sapiens"
 /strain="Homo sapiens"
 /clone="DREF2434N1917"
 /library="CDNA"
 /tissue_type="testis"
 /dev_stage="100 days"
 /lab_host="DH10B"
 /note="Vector: pSport1; Site 1: NotI; Site 2: SalI"

FEATURES

Location/Qualifiers
 1. 387
 /organism="Homo sapiens"
 /strain="Homo sapiens"
 /clone="DREF2434N1917"
 /library="CDNA"
 /tissue_type="testis"
 /dev_stage="100 days"
 /lab_host="DH10B"
 /note="Vector: pSport1; Site 1: NotI; Site 2: SalI"

BASE COUNT

63 a 0.4% Score 21: DB 28: Length 387:
 104 c 0.1%
 103 g 0.1%
 117 t 0.1%

Query Match 0.4% Score 21: DB 28: Length 387:
 Best Local Similarity 100.0% Pred. No. 71:
 Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Query Match 0.4% Score 21: DB 91: Length 391:
 Best Local Similarity 100.0% Pred. No. 71:
 Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Oy 382 attcaagaaagaaaaaa 402
 Db 24 ATTATCAAAAATAAAAAA 4
 RESULT 43
 A1132821 400 bp mRNA EST 27-NOV-1996
 DEFINITION IMAGE:587235.5', mRNA sequence.
 ACCESSION A1132821
 VERSION A1132821.1 GI:1694310
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 400)
 Hillier, L., Lomen, G., Becker, M., Bonaldo, M.F., Chapell, B.,
 Chisore, S., Dietrich, N., Dubugre, T., Favello, A., Glan, H., Hawkins,
 M., Hillman, M., Kucan, T., Lacey, J., Le, M., Le, N., Martin, E., Moore,
 Schellberg, K., Soares, M.B., Tan, F., Thier, D., Trevisan, E.,
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Hare, M.
 Generation and analysis of 280,000 human expressed sequence tags
 genome Res. 6 (9), 807-828 (1996)
 CONTACT: Wilson, R.K.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

QY 2403 ttctggagaagaagtcagagaa 2432
Db 310 ttttgcacaaacacgtacacacaa 310

RESULT 50
LOCUS B9513151 413 bp. mRNA EST 04-OCT-2000
DEFINITION UT-H-CCO a2x-9-02-0-UI 2 NR_HBMF Ref1 Mus muscular cDNA clone
ACCESSION B9513151 UT-H-CCO a2x-9-02-0-UI-3, mRNA sequence.
VERSION B9513151.1 GI:10550686
KEYWORDS EST
SOURCE house mouse
ORGANISM Mus musculus
TAXID 10116
OTHER DBS
REFERENCE 1 Bonaldi, M.P., Lemmon, G., and Soares, M.B.
AUTHORS Normalization and subtraction: two approaches to facilitate gene
TITLE Genomic Res. 6 (9), 791-806 (1996)
JOURNAL 97044477
MEDLINE
COMMENT Contact: Chih, H
Molecular Institute of Mental Health
6501 University Avenue, Room H-1550, MHC 9643, Berkeley, MD
20892-9643, USA
E-mail: hchih@uic.edu
Tel.: 301.443.9850
Fax: 301.443.1706
The sequence contains an oligo-dT track that was present in the
sequence submitted. The sequence was confirmed by sequencing the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonaldi poly A
tail. The sequence was present in the cDNA between the NotI site
and the HindIII site. The sequence was also present in the cDNA
clone distribution. Researchers may obtain BMAP cDNA clones from
RSCMH GENOTEC. It should be noted that Bonto Soares is a
member of the Soares laboratory. The BMAP cDNA clones contain an
array of BMAP cDNAs whose availability will be considered under
appropriate and limited collaborative arrangements. The following
repetitive elements were found in this cDNA sequence: 29-74,
5'cd primer: NA3 forward
POLY(A)Tcs.

FEATURES
source location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/Gene="UT-H-CCO-a2x-9-02-0-UI"

[illegible]

Mar 17 09:22:21 2001
 us-09-410-835-4-0.019.rat
 High quality sequence atop: 351
 Source: IMAGE Consortium (LML)
 This clone is available royalty-free through LML ; contact the
 IMAGE Consortium (envirolang@lml.gov) for further information
 Insert Length: 384 Std Error: 0.00
 High quality sequence atop: 251.
 Location/Qualifiers
 1..415

REFERENCE	1 (base 1 to 419)
AUTHORS	Barnes R.D., Grossman S.D., Rhoads D., Dasg S., Elmer K., Golden K., Hartley J.L., Hsu C.S.H., Kozlowski L., Lohr G.C.
TITLE	Determining DNA End Sequences for Sequence Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other-Access: NCBI1+EMBL2.TK
	Department of Eukaryotic Genomics The Institute for Genomic Research

```

Query Match      0.43; Score 21; DB 144; Length 415;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY      389 aaaaaaaaaaaatgcttga 409
      |||||||
Db      47 aaaaaaaaaaaatgcttga 27

RESULT# 52
AO198451
LOCUS      AO198451      419 bp      DNA
DEFINITION R0C111-48W22_T3 R0C111 Homo sapiens genomic clone R0C111-48W22.
ACCESSION AO198451
VERSION 1
KEYWORDS  GSS
SOURCE      human.
ORGANISM   Homo sapiens
            Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

	<div style="text-align:center;">Spcll Human Male BMC Library</div>					
BASE COUNT			78 c	60 g 120 t		
ORIGIN						
	161 a					
Query Match			0.4%	Score 21:	NB 150;	
Best Local Similarity			100.0%:	Pred.	No. 71;	
Matches	21:	Conservative	0;	Mismatches	0; Indels	
			0;	Gaps	0	
Oy	383	ttattgagaaataaaaaaat	403			
		ttaaaaaaaaaaaaat	403			
Dd	181	TGATGGAGGAAGAATAAAT	201			
RESULT 53						
AAMJ21430		43 bp	RNA		ESE	
DEFINITION	uc011092.y1 NC_054674 Mus musculus cpna clone IMAGE:801122.5'					
ACCESSION	AAMJ21430					
VERSION	AAMJ21430.1	GI:6750974				

AUTIIONS	Journet,E.P., Crespeau,H.,van-Thien,D.,Gouzy,J.,Jallion,O.,Nebel,A.,Circieu-V.,Chagnier,O.,Kohn D., Glahnaxiz-Beardon A. and Gams P.
TITLE	Isolation of cDNA ESTs from nitrogen-starved roots
JOURNAL	Molecular Plant-Microbe Interactions
COMMENT	Unpublished (2000)
Contact:	Genoscope Centre National de Sequencage Genoscope, 21 place du Dr R. Brice, 91060 Evry-Courcouronnes, France. E-mail: acquies@genoscope.cns.fr Web : www.genoscope.cns.fr Contact : Pascal Gams and Etienne-Pascal Journet, Laboratoire de Biologie Moleculaire des Relations Plantes-Microorganismes, INRA UR 87 1316 Castanet-Nolan Cedex, France (Email : p.gams@nolan.inra.fr; e.journet@nolan.inra.fr) http://sequence.toulouse.inra.fr/Miscuneula.html .
FEATURES	Location/Qualifiers
source	1..440 mas="Medicago truncatula" "cultivar:"semalong" "/cellular:"xenolog" /db_xref="taxon:3880" /cclone="MBA27P02" /tissue_type="root tips" /dev_stage="harvested after 3 days of N starvation" /note="Vector: pBluescript pSK. Site_1: EcoRI; Site_2: XbaI. Plants were grown in an aeroponic chamber for 14 d in dark. RNA was extracted from root tips (1-3 cm) in RNAlater medium. RNA was extracted from root tips (1-3 cm). cDNA was prepared from poly(A)-enriched RNA. The cDNA was directionally ligated into Uni-ZapR vector from BamHI-XbaI sites. The library was screened by hybridizing msa-extracted from phase stocks using EcaESTs vernal extracts. Plasmids containing cDNA inserts were electroporated in Salk cells. Clone excising and propagation in Salk cells. Clone screening at Genoscope (Genoscope, Evry, France)." 128 t
BASE COUNT	154 a 97 c 66 g 28 t
ORIGIN	
Query Match	0.4%; Score 21; GS 28; Length 440;
Best Local Similarity	100.0%; Pred. No. 71;
Matches 21:	Conservative 0; Mismatches 0;
Oy	382 attatagaagaaaaaaa 402
Db	12 ATTTATCAAAAAAAAAA 12
RESULT 61	
A142594/c	
442 bp	mRNA
EST	05-MAR-1999

Tue Mar 27 09:32:21 200

us-09-410-835-4.01hg.rst

Page 103

[illegible][illegible]

Tue Mar 27 09:32:21 2001

us-09-410-835-4.011g.rst

Page 104

```

Seq primer: M13 forward
          POLY-TCGA
          source
          448
          Location/Qualifiers
              /organism="Mus musculus"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /date="2006-07-07"
              /library="NIH-BMMP-Ref1.N"
              /dev="steer"
              /size="13.5 days pc"
              /lab="Joc-Biol08 (Life Technologies)"
              /polymerase="Sili1.N"
              /polymerase="Sili1.N; Sili2.N; Sili3.N; Sili4.N; Sili5.N; Sili6.N; Sili7.N; Sili8.N; Sili9.N; Sili10.N; Sili11.N; Sili12.N; Sili13.N; Sili14.N; Sili15.N; Sili16.N; Sili17.N; Sili18.N; Sili19.N; Sili20.N; Sili21.N; Sili22.N; Sili23.N; Sili24.N; Sili25.N; Sili26.N; Sili27.N; Sili28.N; Sili29.N; Sili30.N; Sili31.N; Sili32.N; Sili33.N; Sili34.N; Sili35.N; Sili36.N; Sili37.N; Sili38.N; Sili39.N; Sili40.N; Sili41.N; Sili42.N; Sili43.N; Sili44.N; Sili45.N; Sili46.N; Sili47.N; Sili48.N; Sili49.N; Sili50.N; Sili51.N; Sili52.N; Sili53.N; Sili54.N; Sili55.N; Sili56.N; Sili57.N; Sili58.N; Sili59.N; Sili60.N; Sili61.N; Sili62.N; Sili63.N; Sili64.N; Sili65.N; Sili66.N; Sili67.N; Sili68.N; Sili69.N; Sili70.N; Sili71.N; Sili72.N; Sili73.N; Sili74.N; Sili75.N; Sili76.N; Sili77.N; Sili78.N; Sili79.N; Sili80.N; Sili81.N; Sili82.N; Sili83.N; Sili84.N; Sili85.N; Sili86.N; Sili87.N; Sili88.N; Sili89.N; Sili90.N; Sili91.N; Sili92.N; Sili93.N; Sili94.N; Sili95.N; Sili96.N; Sili97.N; Sili98.N; Sili99.N; Sili100.N; Sili101.N; Sili102.N; Sili103.N; Sili104.N; Sili105.N; Sili106.N; Sili107.N; Sili108.N; Sili109.N; Sili110.N; Sili111.N; Sili112.N; Sili113.N; Sili114.N; Sili115.N; Sili116.N; Sili117.N; Sili118.N; Sili119.N; Sili120.N; Sili121.N; Sili122.N; Sili123.N; Sili124.N; Sili125.N; Sili126.N; Sili127.N; Sili128.N; Sili129.N; Sili130.N; Sili131.N; Sili132.N; Sili133.N; Sili134.N; Sili135.N; Sili136.N; Sili137.N; Sili138.N; Sili139.N; Sili140.N; Sili141.N; Sili142.N; Sili143.N; Sili144.N; Sili145.N; Sili146.N; Sili147.N; Sili148.N; Sili149.N; Sili150.N; Sili151.N; Sili152.N; Sili153.N; Sili154.N; Sili155.N; Sili156.N; Sili157.N; Sili158.N; Sili159.N; Sili160.N; Sili161.N; Sili162.N; Sili163.N; Sili164.N; Sili165.N; Sili166.N; Sili167.N; Sili168.N; Sili169.N; Sili170.N; Sili171.N; Sili172.N; Sili173.N; Sili174.N; Sili175.N; Sili176.N; Sili177.N; Sili178.N; Sili179.N; Sili180.N; Sili181.N; Sili182.N; Sili183.N; Sili184.N; Sili185.N; Sili186.N; Sili187.N; Sili188.N; Sili189.N; Sili190.N; Sili191.N; Sili192.N; Sili193.N; Sili194.N; Sili195.N; Sili196.N; Sili197.N; Sili198.N; Sili199.N; Sili200.N; Sili201.N; Sili202.N; Sili203.N; Sili204.N; Sili205.N; Sili206.N; Sili207.N; Sili208.N; Sili209.N; Sili210.N; Sili211.N; Sili212.N; Sili213.N; Sili214.N; Sili215.N; Sili216.N; Sili217.N; Sili218.N; Sili219.N; Sili220.N; Sili221.N; Sili222.N; Sili223.N; Sili224.N; Sili225.N; Sili226.N; Sili227.N; Sili228.N; Sili229.N; Sili230.N; Sili231.N; Sili232.N; Sili233.N; Sili234.N; Sili235.N; Sili236.N; Sili237.N; Sili238.N; Sili239.N; Sili240.N; Sili241.N; Sili242.N; Sili243.N; Sili244.N; Sili245.N; Sili246.N; Sili247.N; Sili248.N; Sili249.N; Sili250.N; Sili251.N; Sili252.N; Sili253.N; Sili254.N; Sili255.N; Sili256.N; Sili257.N; Sili258.N; Sili259.N; Sili260.N; Sili261.N; Sili262.N; Sili263.N; Sili264.N; Sili265.N; Sili266.N; Sili267.N; Sili268.N; Sili269.N; Sili270.N; Sili271.N; Sili272.N; Sili273.N; Sili274.N; Sili275.N; Sili276.N; Sili277.N; Sili278.N; Sili279.N; Sili280.N; Sili281.N; Sili282.N; Sili283.N; Sili284.N; Sili285.N; Sili286.N; Sili287.N; Sili288.N; Sili289.N; Sili290.N; Sili291.N; Sili292.N; Sili293.N; Sili294.N; Sili295.N; Sili296.N; Sili297.N; Sili298.N; Sili299.N; Sili300.N; Sili301.N; Sili302.N; Sili303.N; Sili304.N; Sili305.N; Sili306.N; Sili307.N; Sili308.N; Sili309.N; Sili310.N; Sili311.N; Sili312.N; Sili313.N; Sili314.N; Sili315.N; Sili316.N; Sili317.N; Sili318.N; Sili319.N; Sili320.N; Sili321.N; Sili322.N; Sili323.N; Sili324.N; Sili325.N; Sili326.N; Sili327.N; Sili328.N; Sili329.N; Sili330.N; Sili331.N; Sili332.N; Sili333.N; Sili334.N; Sili335.N; Sili336.N; Sili337.N; Sili338.N; Sili339.N; Sili340.N; Sili341.N; Sili342.N; Sili343.N; Sili344.N; Sili345.N; Sili346.N; Sili347.N; Sili348.N; Sili349.N; Sili350.N; Sili351.N; Sili352.N; Sili353.N; Sili354.N; Sili355.N; Sili356.N; Sili357.N; Sili358.N; Sili359.N; Sili360.N; Sili361.N; Sili362.N; Sili363.N; Sili364.N; Sili365.N; Sili366.N; Sili367.N; Sili368.N; Sili369.N; Sili370.N; Sili371.N; Sili372.N; Sili373.N; Sili374.N; Sili375.N; Sili376.N; Sili377.N; Sili378.N; Sili379.N; Sili380.N; Sili381.N; Sili382.N; Sili383.N; Sili384.N; Sili385.N; Sili386.N; Sili387.N; Sili388.N; Sili389.N; Sili390.N; Sili391.N; Sili392.N; Sili393.N; Sili394.N; Sili395.N; Sili396.N; Sili397.N; Sili398.N; Sili399.N; Sili400.N; Sili401.N; Sili402.N; Sili403.N; Sili404.N; Sili405.N; Sili406.N; Sili407.N; Sili408.N; Sili409.N; Sili410.N; Sili411.N; Sili412.N; Sili413.N; Sili414.N; Sili415.N; Sili416.N; Sili417.N; Sili418.N; Sili419.N; Sili420.N; Sili421.N; Sili422.N; Sili423.N; Sili424.N; Sili425.N; Sili426.N; Sili427.N; Sili428.N; Sili429.N; Sili430.N; Sili431.N; Sili432.N; Sili433.N; Sili434.N; Sili435.N; Sili436.N; Sili437.N; Sili438.N; Sili439.N; Sili440.N; Sili441.N; Sili442.N; Sili443.N; Sili444.N; Sili445.N; Sili446.N; Sili447.N; Sili448.N; Sili449.N; Sili450.N; Sili451.N; Sili452.N; Sili453.N; Sili454.N; Sili455.N; Sili456.N; Sili457.N; Sili458.N; Sili459.N; Sili460.N; Sili461.N; Sili462.N; Sili463.N; Sili464.N; Sili465.N; Sili466.N; Sili467.N; Sili468.N; Sili469.N; Sili470.N; Sili471.N; Sili472.N; Sili473.N; Sili474.N; Sili475.N; Sili476.N; Sili477.N; Sili478.N; Sili479.N; Sili480.N; Sili481.N; Sili482.N; Sili483.N; Sili484.N; Sili485.N; Sili486.N; Sili487.N; Sili488.N; Sili489.N; Sili490.N; Sili491.N; Sili492.N; Sili493.N; Sili494.N; Sili495.N; Sili496.N; Sili497.N; Sili498.N; Sili499.N; Sili500.N; Sili501.N; Sili502.N; Sili503.N; Sili504.N; Sili505.N; Sili506.N; Sili507.N; Sili508.N; Sili509.N; Sili510.N; Sili511.N; Sili512.N; Sili513.N; Sili514.N; Sili515.N; Sili516.N; Sili517.N; Sili518.N; Sili519.N; Sili520.N; Sili521.N; Sili522.N; Sili523.N; Sili524.N; Sili525.N; Sili526.N; Sili527.N; Sili528.N; Sili529.N; Sili530.N; Sili531.N; Sili532.N; Sili533.N; Sili534.N; Sili535.N; Sili536.N; Sili537.N; Sili538.N; Sili539.N; Sili540.N; Sili541.N; Sili542.N; Sili543.N; Sili544.N; Sili545.N; Sili546.N; Sili547.N; Sili548.N; Sili549.N; Sili550.N; Sili551.N; Sili552.N; Sili553.N; Sili554.N; Sili555.N; Sili556.N; Sili557.N; Sili558.N; Sili559.N; Sili560.N; Sili561.N; Sili562.N; Sili563.N; Sili564.N; Sili565.N; Sili566.N; Sili567.N; Sili568.N; Sili569.N; Sili570.N; Sili571.N; Sili572.N; Sili573.N; Sili574.N; Sili575.N; Sili576.N; Sili577.N; Sili578.N; Sili
```


SOURCE Human.
ORGANISM Human.
REFERENCE 1 (bases 1 to 511)
AUTHORS Mahaira C.G., Wallace J.C., Smith F., Swartzell S., Holman F., Hood L., Shaker A., Furlong J., Tong J., Zhao S., Adams M.D. and
TITLE Scanning the human genome: A sequence approach to mapping and
JOURNAL Genome Res. 9:1058-1068 (1999)
COMMENT Contact: Mahaira C.G., Wallace J.C., Hood L.
University of Washington
High Throughput Sequencing Center
420 University of Washington
Box 357350
Seattle, WA 98195, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence tagged connector
Accession: U00584
Class: BAC ends
High quality sequence stop: 511.
Location/Qualifiers
1. 511
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIR Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
BASE COUNT 158 a 103 c 125 g 125 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 21; DB 150; Length 511;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 406 AAAAAAAAAAAATCTCTTA 426
RESULT 79
AL35814 513 bp mRNA EST
LOCUS AL35814.1 MIMC Medicago truncatula cDNA clone MIMC0012.77, mRNA
DEFINITION sequence
ACCESSION AL35814

Tue Mar 27 09:32:21 2001

us-09-410-835-4.o11g.txt

Page 127

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 21; DB 28; Length 513;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 482 ATTATGAAAAAATAA 502
RESULT 80
AC096044 519 bp mRNA EST
LOCUS AC096044.1 Rice green shoot Oryza sativa cDNA clone 51953, mRNA
DEFINITION sequence
ACCESSION AC096044.1 GI:8659726
VERSION 1.0
KEYWORDS Oryza sativa
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1
AUTHORS Sakaki T. and Yano K.
TITLE Rice cDNA from green shoot (2000)
JOURNAL Unpublished (2000)
COMMENT Contact: Takaji Sakaki
National Institute of Agricultural Resources
2-1-2 Kamondai, Tsukuba
Ibaraki, 305
Japan
Tel: 0285-38-7441
Fax: 0285-38-7468
Email: tanaaki@affrc.go.jp
PROJECT "RGP"
51953.102 Location/Qualifiers
1. 519
/organism="Oryza sativa"
/strain="Nipponbare"
/db_xref="taxon:9306"
/clone_lib="Rice green shoot"
/note="Green shoot (8 days old)"
BASE COUNT 135 a 147 c 121 g 113 t 2 others
ORIGIN

Tue Mar 27 09:32:21 2001

us-09-410-835-4.o11g.txt

Page 126

VERSION AL35814.1 GI:9685565
REMARKS EST from MIMC
ORGANISM Medicago truncatula
REFERENCE 1
AUTHORS Mahaira C.G., Wallace J.C., Smith F., Swartzell S., Holman F., Hood L., Shaker A., Furlong J., Tong J., Zhao S., Adams M.D. and
TITLE Scanning the human genome: A sequence approach to mapping and
JOURNAL Genome Res. 9:1058-1068 (1999)
COMMENT Contact: Mahaira C.G., Wallace J.C., Hood L.
University of Washington
High Throughput Sequencing Center
420 University of Washington
Box 357350
Seattle, WA 98195, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence tagged connector
Accession: U00584
Class: BAC ends
High quality sequence stop: 511.
Location/Qualifiers
1. 513
/organism="Medicago truncatula"
/strain="J163"
/db_xref="taxon:3180"
/clone_lib="MIMC"
/clone_lib="MIMC"
/note="Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
BASE COUNT 162 a 131 c 123 g 130 t

Tue Mar 27 09:32:21 2001

us-09-410-835-4.o11g.txt

Page 128

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 21; DB 29; Length 519;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 483 ATTATGAAAAAATAA 503
RESULT 81
AA32599/c 522 bp mRNA EST
LOCUS AA32599.1 MIMC Medicago truncatula cDNA clone
DEFINITION sequence
ACCESSION AA32599.1 GI:3906127
VERSION 1.0
KEYWORDS Medicago truncatula
SOURCE Medicago truncatula
ORGANISM Medicago truncatula
REFERENCE 1
AUTHORS Mahaira C.G., Wallace J.C., Smith F., Swartzell S., Holman F., Hood L., Shaker A., Furlong J., Tong J., Zhao S., Adams M.D. and
TITLE Scanning the human genome: A sequence approach to mapping and
JOURNAL Genome Res. 9:1058-1068 (1999)
COMMENT Contact: Mahaira C.G., Wallace J.C., Hood L.
University of Washington
High Throughput Sequencing Center
420 University of Washington
Box 357350
Seattle, WA 98195, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence tagged connector
Accession: U00584
Class: BAC ends
High quality sequence stop: 511.
Location/Qualifiers
1. 522
/organism="Medicago truncatula"
/strain="J163"
/db_xref="taxon:3180"
/clone_lib="MIMC"
/clone_lib="MIMC"
/note="Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
BASE COUNT 162 a 131 c 123 g 130 t

[illegible]

Tue May 27 09:32:21 2001

us-09-410-835-4.01lg.rst

Page 143

TUE MAR 27 09:32:21 2001

us-09-410-835-4.011g.rst

Page 144

```

REFERENCE      2 (bases 1 to 669)
AUTHORS       Roest-Collins,R., Jallion,O., Davila,C., Bouneau,L., Flater,C.,
              Smith,M., and Weissbach,J.,Xer,P., Bortier,F., Queller,F.,
              Human gene number estimate provided by genome wide analysis using
TITLE          Tetrodon nigroviridis DNA sequence
JOURNAL       unpublished
REFERENCE     1 to 669)
AUTHORS       Genoscope.
FEATURES      Location/Qualifiers
              source
              /organism="Tetrodon nigroviridis"
              /db_xref="taxon:99883"
              /clone="01710"
              /mol_type="genomic DNA"
              /accession="AF049114"
              /version="1"
              /rebase="1"
              /project="Genoscope"
              /map="Genoscope"
              /contig="Genoscope"
              /contig_start="1"
              /contig_end="669"
              /contig_size="669"
              /contig_type="genomic"
              /contig_status="new"
              /contig_date="1998-01-01"
              /contig_author="Genoscope"
              /contig_contact="Genoscope"
              /contig_email="Genoscope"
              /contig_phone="Genoscope"
              /contig_fax="Genoscope"
              /contig_url="Genoscope"
              /contig_address="Genoscope"
              /contig_city="Genoscope"
              /contig_state="Genoscope"
              /contig_country="Genoscope"
              /contig_postcode="Genoscope"
              /contig_zip="Genoscope"
              /contig_zip2="Genoscope"
              /contig_zip3="Genoscope"
              /contig_zip4="Genoscope"
              /contig_zip5="Genoscope"
              /contig_zip6="Genoscope"
              /contig_zip7="Genoscope"
              /contig_zip8="Genoscope"
              /contig_zip9="Genoscope"
              /contig_zip10="Genoscope"
              /contig_zip11="Genoscope"
              /contig_zip12="Genoscope"
              /contig_zip13="Genoscope"
              /contig_zip14="Genoscope"
              /contig_zip15="Genoscope"
              /contig_zip16="Genoscope"
              /contig_zip17="Genoscope"
              /contig_zip18="Genoscope"
              /contig_zip19="Genoscope"
              /contig_zip20="Genoscope"
              /contig_zip21="Genoscope"
              /contig_zip22="Genoscope"
              /contig_zip23="Genoscope"
              /contig_zip24="Genoscope"
              /contig_zip25="Genoscope"
              /contig_zip26="Genoscope"
              /contig_zip27="Genoscope"
              /contig_zip28="Genoscope"
              /contig_zip29="Genoscope"
              /contig_zip30="Genoscope"
              /contig_zip31="Genoscope"
              /contig_zip32="Genoscope"
              /contig_zip33="Genoscope"
              /contig_zip34="Genoscope"
              /contig_zip35="Genoscope"
              /contig_zip36="Genoscope"
              /contig_zip37="Genoscope"
              /contig_zip38="Genoscope"
              /contig_zip39="Genoscope"
              /contig_zip40="Genoscope"
              /contig_zip41="Genoscope"
              /contig_zip42="Genoscope"
              /contig_zip43="Genoscope"
              /contig_zip44="Genoscope"
              /contig_zip45="Genoscope"
              /contig_zip46="Genoscope"
              /contig_zip47="Genoscope"
              /contig_zip48="Genoscope"
              /contig_zip49="Genoscope"
              /contig_zip50="Genoscope"
              /contig_zip51="Genoscope"
              /contig_zip52="Genoscope"
              /contig_zip53="Genoscope"
              /contig_zip54="Genoscope"
              /contig_zip55="Genoscope"
              /contig_zip56="Genoscope"
              /contig_zip57="Genoscope"
              /contig_zip58="Genoscope"
              /contig_zip59="Genoscope"
              /contig_zip60="Genoscope"
              /contig_zip61="Genoscope"
              /contig_zip62="Genoscope"
              /contig_zip63="Genoscope"
              /contig_zip64="Genoscope"
              /contig_zip65="Genoscope"
              /contig_zip66="Genoscope"
              /contig_zip67="Genoscope"
              /contig_zip68="Genoscope"
              /contig_zip69="Genoscope"
              /contig_zip70="Genoscope"
              /contig_zip71="Genoscope"
              /contig_zip72="Genoscope"
              /contig_zip73="Genoscope"
              /contig_zip74="Genoscope"
              /contig_zip75="Genoscope"
              /contig_zip76="Genoscope"
              /contig_zip77="Genoscope"
              /contig_zip78="Genoscope"
              /contig_zip79="Genoscope"
              /contig_zip80="Genoscope"
              /contig_zip81="Genoscope"
              /contig_zip82="Genoscope"
              /contig_zip83="Genoscope"
              /contig_zip84="Genoscope"
              /contig_zip85="Genoscope"
              /contig_zip86="Genoscope"
              /contig_zip87="Genoscope"
              /contig_zip88="Genoscope"
              /contig_zip89="Genoscope"
              /contig_zip90="Genoscope"
              /contig_zip91="Genoscope"
              /contig_zip92="Genoscope"
              /contig_zip93="Genoscope"
              /contig_zip94="Genoscope"
              /contig_zip95="Genoscope"
              /contig_zip96="Genoscope"
              /contig_zip97="Genoscope"
              /contig_zip98="Genoscope"
              /contig_zip99="Genoscope"
              /contig_zip100="Genoscope"
              /contig_zip101="Genoscope"
              /contig_zip102="Genoscope"
              /contig_zip103="Genoscope"
              /contig_zip104="Genoscope"
              /contig_zip105="Genoscope"
              /contig_zip106="Genoscope"
              /contig_zip107="Genoscope"
              /contig_zip108="Genoscope"
              /contig_zip109="Genoscope"
              /contig_zip110="Genoscope"
              /contig_zip111="Genoscope"
              /contig_zip112="Genoscope"
              /contig_zip113="Genoscope"
              /contig_zip114="Genoscope"
              /contig_zip115="Genoscope"
              /contig_zip116="Genoscope"
              /contig_zip117="Genoscope"
              /contig_zip118="Genoscope"
              /contig_zip119="Genoscope"
              /contig_zip120="Genoscope"
              /contig_zip121="Genoscope"
              /contig_zip122="Genoscope"
              /contig_zip123="Genoscope"
              /contig_zip124="Genoscope"
              /contig_zip125="Genoscope"
              /contig_zip126="Genoscope"
              /contig_zip127="Genoscope"
              /contig_zip128="Genoscope"
              /contig_zip129="Genoscope"
              /contig_zip130="Genoscope"
              /contig_zip131="Genoscope"
              /contig_zip132="Genoscope"
              /contig_zip133="Genoscope"
              /contig_zip134="Genoscope"
              /contig_zip135="Genoscope"
              /contig_zip136="Genoscope"
              /contig_zip137="Genoscope"
              /contig_zip138="Genoscope"
              /contig_zip139="Genoscope"
              /contig_zip140="Genoscope"
              /contig_zip141="Genoscope"
              /contig_zip142="Genoscope"
              /contig_zip143="Genoscope"
              /contig_zip144="Genoscope"
              /contig_zip145="Genoscope"
              /contig_zip146="Genoscope"
              /contig_zip147="Genoscope"
              /contig_zip148="Genoscope"
              /contig_zip149="Genoscope"
              /contig_zip150="Genoscope"
              /contig_zip151="Genoscope"
              /contig_zip152="Genoscope"
              /contig_zip153="Genoscope"
              /contig_zip154="Genoscope"
              /contig_zip155="Genoscope"
              /contig_zip156="Genoscope"
              /contig_zip157="Genoscope"
              /contig_zip158="Genoscope"
              /contig_zip159="Genoscope"
              /contig_zip160="Genoscope"
              /contig_zip161="Genoscope"
              /contig_zip162="Genoscope"
              /contig_zip163="Genoscope"
              /contig_zip164="Genoscope"
              /contig_zip165="Genoscope"
              /contig_zip166="Genoscope"
              /contig_zip167="Genoscope"
              /contig_zip168="Genoscope"
              /contig_zip169="Genoscope"
              /contig_zip170="Genoscope"
              /contig_zip171="Genoscope"
              /contig_zip172="Genoscope"
              /contig_zip173="Genoscope"
              /contig_zip174="Genoscope"
              /contig_zip175="Genoscope"
              /contig_zip176="Genoscope"
              /contig_zip177="Genoscope"
              /contig_zip178="Genoscope"
              /contig_zip179="Genoscope"
              /contig_zip180="Genoscope"
              /contig_zip181="Genoscope"
              /contig_zip182="Genoscope"
              /contig_zip183="Genoscope"
              /contig_zip184="Genoscope"
              /contig_zip185="Genoscope"
              /contig_zip186="Genoscope"
              /contig_zip187="Genoscope"
              /contig_zip188="Genoscope"
              /contig_zip189="Genoscope"
              /contig_zip190="Genoscope"
              /contig_zip191="Genoscope"
              /contig_zip192="Genoscope"
              /contig_zip193="Genoscope"
              /contig_zip194="Genoscope"
              /contig_zip195="Genoscope"
              /contig_zip196="Genoscope"
              /contig_zip197="Genoscope"
              /contig_zip198="Genoscope"
              /contig_zip199="Genoscope"
              /contig_zip200="Genoscope"
              /contig_zip201="Genoscope"
              /contig_zip202="Genoscope"
              /contig_zip203="Genoscope"
              /contig_zip204="Genoscope"
              /contig_zip205="Genoscope"
              /contig_zip206="Genoscope"
              /contig_zip207="Genoscope"
              /contig_zip208="Genoscope"
              /contig_zip209="Genoscope"
              /contig_zip210="Genoscope"
              /contig_zip211="Genoscope"
              /contig_zip212="Genoscope"
              /contig_zip213="Genoscope"
              /contig_zip214="Genoscope"
              /contig_zip215="Genoscope"
              /contig_zip216="Genoscope"
              /contig_zip217="Genoscope"
              /contig_zip218="Genoscope"
              /contig_zip219="Genoscope"
              /contig_zip220="Genoscope"
              /contig_zip221="Genoscope"
              /contig_zip222="Genoscope"
              /contig_zip223="Genoscope"
              /contig_zip224="Genoscope"
              /contig_zip225="Genoscope"
              /contig_zip226="Genoscope"
              /contig_zip227="Genoscope"
              /contig_zip228="Genoscope"
              /contig_zip229="Genoscope"
              /contig_zip230="Genoscope"
              /contig_zip231="Genoscope"
              /contig_zip232="Genoscope"
              /contig_zip233="Genoscope"
              /contig_zip234="Genoscope"
              /contig_zip235="Genoscope"
              /contig_zip236="Genoscope"
              /contig_zip237="Genoscope"
              /contig_zip238="Genoscope"
              /contig_zip239="Genoscope"
              /contig_zip240="Genoscope"
              /contig_zip241="Genoscope"
              /contig_zip242="Genoscope"
              /contig_zip243="Genoscope"
              /contig_zip244="Genoscope"
              /contig_zip245="Genoscope"
              /contig_zip246="Genoscope"
              /contig_zip247="Genoscope"
              /contig_zip248="Genoscope"
              /contig_zip249="Genoscope"
              /contig_zip250="Genoscope"
              /contig_zip251="Genoscope"
              /contig_zip252="Genoscope"
              /contig_zip253="Genoscope"
              /contig_zip254="Genoscope"
              /contig_zip255="Genoscope"
              /contig_zip256="Genoscope"
              /contig_zip257="Genoscope"
              /contig_zip258="Genoscope"
              /contig_zip259="Genoscope"
              /contig_zip260="Genoscope"
              /contig_zip261="Genoscope"
              /contig_zip262="Genoscope"
              /contig_zip263="Genoscope"
              /contig_zip264="Genoscope"
              /contig_zip265="Genoscope"
              /contig_zip266="Genoscope"
              /contig_zip267="Genoscope"
              /contig_zip268="Genoscope"
              /contig_zip269="Genoscope"
              /contig_zip270="Genoscope"
              /contig_zip271="Genoscope"
              /contig_zip272="Genoscope"
              /contig_zip273="Genoscope"
              /contig_zip274="Genoscope"
              /contig_zip275="Genoscope"
              /contig_zip276="Genoscope"
              /contig_zip277="Genoscope"
              /contig_zip278="Genoscope"
              /contig_zip279="Genoscope"
              /contig_zip280="Genoscope"
              /contig_zip281="Genoscope"
              /contig_zip282="Genoscope"
              /contig_zip283="Genoscope"
              /contig_zip284="Genoscope"
              /contig_zip285="Genoscope"
              /contig_zip286="Genoscope"
              /contig_zip287="Genoscope"
              /contig_zip288="Genoscope"
              /contig_zip289="Genoscope"
              /contig_zip290="Genoscope"
              /contig_zip291="Genoscope"
              /contig_zip292="Gen
```

TUE MAR 27 09:32:21 2001

us-09-410-835-4.011g.rst

Page 144

JOURNAL
Unpublished (1997)
Other GSSs: RPCI-11-265118-TV
The National Human Genome Research Institute
Department of Biotechnology Genomics
The Institute for Genetic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 818 0200
Email: bhet@rigi.org

Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieterd@med.buffalo.edu). Clones may be purchased from
Research Center Inc. (<http://www.researchcenter.com>) or from
http://www.tigr.orf.edu/human/bac_end_search/bac_end_search.html.
Seq plaser: s96

Class: BAC-end
GenBank accession/Qualifiers
1..670
/organism='Homo sapiens'
/db_xref='GDB:760158'
/clone_id='RPCI-11-265118'
/clone_1lb='RPCI-11'
/sex='Male'
/cell_type='Lymphocytes'
/map_data='Site-1: EcoRI; Site-2: EcoRI;
Rpci11 Homo Male BAC Library'

COUNT 156 a 168 c 137 g 209 t

ORIGIN

Query Match 0.4% Score 21 DB 160 Length 670;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 21 Conservative 0 Mismatches 0 Indels 0 Gaps 0.
369 aaaaaaaaaaaaaaacgtca 409
|||||iiiiiiiii
Db 319 AAAAAAAAAAATCTTGA 399

RESULT 95
AS2829945
LOCUS AI0382945 692 bp DNA GSS 02-OCT-2000
DEFINITION HMO140C3P clone 10db plasmid UOCCIM library Mus musculus genomic
AI0382945.1 GI:1046645
ACCION AI0382945.1 GI:1046645
VERSION
KEYWORDS house mouse.

Eukaryotes: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Neotoma: Sciurognathi: Muridae: Murinae: Mus.
 Mus. Mus. 036593
 Authors: Dunn, R., Dwyer, B., Rathem, T., Dwyer, B., Rathem, T., Dunn, R., Longaker, S., Mahmoud, K., Meenan, E., Pedersen, T., Rilly, J., Rose, M., Rose, R., Stokes, R., Tinsley, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Title: Mouse mammary gland scaffolding with paired end reads from 10x
 Genomics Hi-C
 Journal: PLoS ONE
 Comment: Unpublished (2000)
 Contact: Robert B. Weiss
 Address: University of Utah Genome Center
 Room 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
 Salt Lake City, UT 84112, USA
 Fax: 801.585.5606
 Fax: 801.585.7177
 Email: rweiss@genome.utah.edu
 Insert Length: 10000
 Plate: 0140 Row: J Column: 23
 Seq primer: GCTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality: 100%
 Location/Qualifiers:
 1..692
 /organism="Mus musculus"
 /db="refseq" /taxid="10090"
 /clone="UUCG14014023"
 /c1one="lib+mouse 10kb plasmid unc010 library"
 /sex="Male"
 /mol="c" /col="strain XL10-cold, m-resistant, F-"
 /note="vector: pMD219; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA was extracted using the QIAzol lysis reagent (Qiagen) and 0.005 inch offices at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerases and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The ligated DNA was then digested with EcoRV. The resulting 10.5 kb DNA range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD21 (g11732119b) (AF129072), a copy-number undetectable derivative of plasmid R1. The vector was ligated with the sheared DNA and ligated into the R1 vector. The ligation was then transformed into competent cells. The cells were then pulsed. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-cold (Stratagene) cells

Query 383 ttaatgagagagagagagagagagag 402
 Db 215 TTAATGAGAGAGAGAGAGAGAGAGAG 214

RESULT 146
 AAI09600 233 bp mRNA EST 20-Oct-1995
 DEFINITION AAI09600.1 CDS for a protein of 710 dpa fiber library
 ACCESSION AAI09600
 VERSION AAI09600.1 GI:6090400
 SOURCE *Oryza sativa*
 ORGANISM *Oryza sativa*
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids II;
 Malvales; Malvaceae; Gossypium
 Authors: Roubtchik, D., Woo, S. S., Wood, T. C., Wing, R. A. and Wilkins
 'T. A., Fitch, D., Woo, S. S., Wood, T. C., Wing, R. A. and Wilkins

TITLE Generation and analysis of 1350 EST's derived from rapidly growing
 JOURNAL *Plant Molecular Biology*
 COMMENT Contact: Wing RA
 Clemson University
 1100 S. State St.
 Clemson, SC 29634, USA
 Tel: 864.656.7288
 Fax: 864.656.4293
 Email: rwing@clemson.edu
 Seq primer: TAAACGACCTACCTACG
 High quality sequence
 Location/Qualifiers
 1..253
 /organism="Gossypium arboreum"
 /strain="AA"
 /db_xref="taxon:59120"
 /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
 /clone_id="Gossypium arboreum 7-10 dpa fiber library"
 /clone_type="Fibers isolated from bolls harvested 7-10
 days after anthesis"
 /lab_host="E. coli"
 /note="Vector: pR-CMV; Site-1: EcoRI; Site-2: XhoI"
 BASE COUNT 91 a 24 c 66 g 72 t
 ORIGIN

Query Match

0.3% Score 20; DB 40; Length 253;

Query Match 0.3% Score 20; DB 38; Length 254;
 Best Local Similarity 100.0%; Pred. No. 2,2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 383 ttaatgagagagagagagagagagag 402
 Db 215 TTAATGAGAGAGAGAGAGAGAGAGAG 214

RESULT 148
 AAI058025 260 bp mRNA EST 29-Apr-1999
 DEFINITION AAI058025.1 Rice callus *Oryza sativa* CDNA C60924_1A, mRNA
 ACCESSION AAI058025
 VERSION AAI058025.1 GI:4714058
 SOURCE EST
 ORGANISM *Oryza sativa*
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza
 Authors: Yamamoto, K. and Sasaki, T.
 Contact: Takuji Sasaki
 National Institute of Agricultural Resources
 1-1-1 Honcho, Tsukuba
 Ibaraki 305
 Japan 305
 Tel: 0298-38-7441
 Fax: 0298-38-7468
 Email: tsasaki@affrc.go.jp
 Project "RDP/Indr. affrc go.jp
 Location/Qualifiers
 1..260
 /organism="Oryza sativa"
 /strain="Callus C60924_1A"
 /db_xref="taxon:4530"
 /clone="C60924_1A"

Best Local Similarity 100.0%; Pred. No. 2,2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2588 ataacttgagagagagagagagagagag 2607
 Db 188 KTAATGAGAGAGAGAGAGAGAGAGAG 189

RESULT 147
 AL168864 254 bp mRNA EST 03-JUN-2000
 DEFINITION M8A27C04R1 M8A Medicago truncatula cDNA clone M8A27C04 77, mRNA
 ACCESSION AL168864
 VERSION AL168864.1 GI:9686617
 SOURCE *Medicago truncatula*
 ORGANISM *Medicago truncatula*
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids I;
 I (bases 1 to 254)
 Authors: Journet, E. P., Crespeau, H., van Toluen, D., Gouy, J., Jallion, O.,
 Journet, E. P., Crespeau, H., van Toluen, D., Gouy, J., Jallion, O.,
 Metel, A., Carreau, V., Chacaguer, O., Kahn, D., Glanville, Pearson
 'A. and Gamas, P.
 Medicago truncatula ESTs from nitrogen-starved roots
 Contact: Genoscope
 Genoscope, Centre National de Sequencage
 BP 11009 GENOTOP
 Evry-Courcouronnes 91000 France
 Email: genoscope@genoscope.cns.fr
 Contact: Pascal Gamas and Etienne Pascal Journet, Laboratoire de
 Biologie Moleculaire des Relations Plantes-Microorganismes,
 CNRS-INRA, BP 27 31926 Castanet-Tolosan Cedex, France (Email :
 http://sequence.toulouse.inra.fr/Medicago.html).

FEATURES

source

1..254
 /organism="Medicago truncatula"
 /strain="M8A27C04"
 /db_xref="taxon:3980"
 /clone="M8A27C04"
 /clone_lib="M8A"
 /clone_id="M8A27C04"
 /clone_type="Root tips"
 /note="Vector: pBluescript pSK; Site-1: EcoRI; Site-2:
 XhoI; Plants were grown in an aeroponic chamber for 14
 days on nitrogen-rich medium followed by 3 days on N-free
 medium. Total RNA was extracted from roots and the cDNA
 was prepared from poly(A) enriched RNA. The cDNA was
 directionally ligated into Uni-ZapXX vector from

Query Match 0.3% Score 20; DB 29; Length 260;
 Best Local Similarity 100.0%; Pred. No. 2,2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 383 ttaatgagagagagagagagagagag 402
 Db 215 TTAATGAGAGAGAGAGAGAGAGAGAG 214

RESULT 149
 AAI08980 261 bp mRNA EST 12-JAN-1999
 DEFINITION AAI08980.1 Soybean L-cystathionase cDNA clone
 1240223.3 similar to contains element PMS repetitive element
 ACCESSION AAI08980
 VERSION AAI08980.1 GI:2849100
 SOURCE EST
 ORGANISM *human*
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Primates; Catarrhini; Hominoidea; Homo
 Authors: NCI-CCAP
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Unpublished (1997)
 Contact: Robert Straube; Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Straube@nih.gov
 Ph.D. Library Preparation: R. Benito Soares, Ph.D., M. Patricia Bonaldo
 CDNA Library Arrayed by: Greg Lammou, Ph.D.
 CDNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCAP clone distribution information can be
 www.bio.101.gov/bnmp/image/image.html
 Insert Length: 1142 Std Error: 0.00
 Seq primer: -40a13 fwd 5' from Amerham
 High quality sequence stop: 188
 Location/Qualifiers
 1..261
 /organism="Oryza sativa"
 /strain="Callus C60924_1A"

[illegible]

Tue Mar 27 09:32:21 2001

us-09-410-835-4.011g.rst

Page 23

Tue Mar 27 09:32:21 200

US-09-410-835-4.0119.rs

Page 23:

CONTACT: Chin, H
National Institute of Mental Health
6000 Executive Blvd. Room 7N-7150, MSC 9643, Bethesda, MD
Tel: 301 443 1106
Fax: 301 443 9890
Email: m57@mail.nih.gov

The sequence contained an oligo-dT track that was present in the strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized brain stems library cDNA Library Preparation: M.B. (National Institute of Mental Health). The cDNA clones will be made available by request. The sequence was determined and this record determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. Seq primer: M3 forward

location/Qualities

FEATURES	Source
1..293	
organism="Mus musculus"	
strain="C57BL/6J"	
clone="H-10-20-0-02-0-01"	
clone_1lib="NIH-BMAP-MBS"	
dev_astg="27-32 days"	
lab_host="DH10 (Life Technologies)"	
polylinker="NotI, XbaI, BamHI, EcoRI, PstI"	
normalized="No"	
NIH-BMAP-MB library is a non-normalized library	
of 5 nucleotides present between the NotI site and the	
oligo-dT track. The library was constructed as described	
in 1996. Tissue provided by Ms. Annie Novakovich,	
State-Willitt Laboratories.	
map_c1lib="BMAP-MBS"	
map_c1lib_descriptor="BMAP-MBS"	
map_c1clone="73-800"	
map_c1clone="74-9"	

```

0.38; Score 25; DB 25; Length 292;
Query Match Similarity 100.0%; PctId. No. 2,2e+02;
Best Local Similarity 100.0%;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 383 TTTATGAAAAAAAAAAAAA 402
DB 23 TTTATGAAAAAAAAAAAAA 4

```

[illegible]

Tue Mar 27 09:32:21 200

US-09-410-835-4.0119.rs

Page 23:

RESULT 163
LOCUS 0096/c
DEFINITION U1-R-10-uV-h-10-O-01-a2 U1-R-YO Ratius novaelegua cDNA clone
ACCESSION A1602026
KEYWORDS EST
SOURCE Norway rat.
ORGANISM Rattus norvegicus
MIMAT009686.1 C1:651187
Mus musculus; Mus musculus; Chondrichna Caninae; Vertebrata; Euteleostomi;
Euteleostomi; Euteleostomi; Rodentia; Sciuromorphi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1294)
AUTHORS Donald M.F., Lemmon G. and Soares M.B.
TITLE Sequence isolation and subtraction: two approaches to facilitate gene
discovery. *Genomics*. 6 (3), 791-806 (1986)
JOURNAL GENOME RESEARCH
MEDLINE 9704447
COMMENT Program for Rat Gene Discovery and Mapping
University of Iowa
451 Engineering Medical Research Building Iowa City, IA 52242, USA
EST 319 335 955
PMID 319 335 955
Email: msoares@vcg.uiowa.edu.

The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
cDNA strand. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
normalised library cDNA library preparation. M.B. Soares Lab
Genetics Univ. iagen.com. The following repetitive elements were
found in this cDNA sequence: 1.27, >AT-richness-complexity
Seq primer: 1.27, >AT-richness-complexity

```
/c/mome.lib=Uir-Yo  
/dev.stgcs=adult  
/lab=epifrontal  
/lib=Technological  
/molecule=Epifrontal  
/polymer: site 1: Pae I; Site 2: Eco RI; The Uir-Yo  
library is a subtracted library derived from an  
individually-tagged normalized whole-eye (minus the lens)
```


FEATURES

- Tissue processing: Chitoseptor Moskatuk, M.D., Ph.D., Michael R. Smoot, Buck, M.D., Ph.D.
- Software: Life Technologies, Inc.
- CDNA Library created by: Greg Lannon, Ph.D.
- DNA Sequencing by: Washington University Genome Sequencing Center
- Clone distribution: NCI/COA clone distribution information can be found at: www.nci.nih.gov/ncicda/clone.htm
- Seq primer: -400P from Gibco
- Location/Qualifiers

```

/organisms Homo sapiens
/db/ncbi/taxon/9606
/clone_id NCICAP_Ga42
/tissue_type poorly_differentiated adenocarcinoma with
  100% tumor cells
/clone_name 0016
/ncbi_organs stomach
/vector pcw-sp076, ste.1, sal.1
/ste.3 nci: cloned undifferentiated, primer: oligo dr
  1154-011
  45 c 133 t

```

```

Query Match Similarity 0.000: Score 20: DB 39: Length 310:
Beat Local 100: Prev. No. 2.2e+02:
Matches 20: Consecutive 0: Mismatches 0: Indels 0: Gaps 0
QY 393 ttaactgaagaaagaaagaaagaa 402
|||||
DB 33 ttaactgaagaaagaaagaaagaa 14

```

RESULTS	BFOI235/c
DEFINITION	BFOI2355 BFS6589YJ Sea-anchored membrane Mus musculus cDNA clone IMAGE:3514155.5, mRNA sequence.
ACCESSION	BFOI2355
VERSION	BFOI2355.1 GI:10712630 .1
REMARKS	EST.
SOURCE ORGANISM	Homo sapiens house mouse
TAXONOMICS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; 1 (base) 1 to 310
REFERENCES	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap/
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Tue Mar 27 09:32:21 2001

us-09-410-835-4.011g.r51

Page 25

Tue Mar 27 09:32:21 200

US-09-410-835-4.011g.r61

Page 25

REFERENCE	1 (bases 1 to 311)
AUTHORS	Bomblao, M.P., Lennon, G. and Soares, M.B.
TITLE	Normalization and substructure: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	97044477
COMMENT	Contact: Chlo. H. National Institute of Mental Health

5000 EXECUTIVE BLVD., ROOM 7N-190, MSC 9643, Bethesda, MD
701.301.443.1706
Fax: 301.443.0990
Email: MES7@mail.nih.gov
01/30/97 track not found, Not a site shown in beginning of sequence
Source: NCBI Clone Distribution: Researchers may obtain BMD CNAs
clones from RESEARCHER GENETICS. It should be noted that Bencio Source
is generating a small number of additional specialized
non-redundant arrays of BMD CNAs whose availability will be
dependent on the availability of the BMD DNA samples.
The following repetitive elements were found in this CNAs sequence:
68-97, >NT_1c10hcv.complexity 250-295, >NT_1c10hcv.complexity
Seq primer: N1 Forward

BASE COUNT
ORIGIN

FEATURES
source

Location/Qualifiers
1. 311
/organism="Mus musculus"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="U1-N-821-B1v-c-12-0-01"
/clone="U1-N-821-B1v-c-12-0-01"
/gene="11b-NIR-BMP-1M12.S1"
/lab="Scgen/CHN03 (Life Technologies)"
/note="Vector: pTZ19-Pac (pharmacia)"
/note="Library: S1c-1; Not 1; S1c-2; Eco RI; The
NIR-BMP-1M12.S1 library is a subtracted library derived
from the NIR-BMP-1M12.NIR-BMP-1M12 is a library derived
from the library from which this clone was derived, please
visit our web site at brainrest.cmg.uiova.edu.
TAC:550-mere found"

103 a 63 c 44 g 101 t

```

      383  ttatgtaaaaaaaaaa 402
      |||
Query Match Similarity 0.38: Score 20: DB 138: Length 311:
Best Local Similarity 100.00: Pct. No. 2:2e+02:
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0
CY

```

Journal Comment
Unpublished (1997)
O'Brien, R. J. 1997. *ax15b07. xl*
O'Brien, R. J. 1997. *ax15b07. ph.d.*
Tel.: (504) 496-1550
Email: Robert_@stansberry. net
This clone is available royalty free through LML; contact the
LML team (lml@stansberry. lml. gov) for further information.
M11.1997035
Seq primer: -468r from Glbo.
Location/Qualifiers

```

/coronaasm - Mus musculus
/cisname - IMAGE 351455
/cisloc - /lib/Genevec.NKWD/ambible*
/ctname - type=ambible
/ncore=vector: pT10D-Pac (Pharmacia) with a modified
polylinker: site: 1: NotI; site: 2: EcoRI; 1st strand cDNA
was placed with a Not I - oligo(dT) primer (5'GTTTCTT 3',
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library

```

BASE COUNT	85 a	57 c	54 g	114 t
ORIGIN				
Query Match	0.31	Score 20:	DB 118:	Length 110:
Best Local Similarity	100.00:	Prod.	2.2e10:	
Matches	20:	Conservative	0:	Models
				0:
				Gaps
				0:

DB	45	TTATGCGAAGAAAAA	26
RESULT 181			
BE95963			
LOCUS	BE95963		
DEFINITION	UT-R-B21-b1-e-12-01-61 nt N18, BM4-MH2.S1 Mus musculus cDNA clone		
ACCESSION	BE95963		
VERSION	BE95963.1		
KEYWORDS	EST		
SOURCE	house mouse		
ORGANISM	Mus musculus		
	Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurimorphi; Muridae; Murinae; Mus.		

Db	271	TTATGAGAAAAAAAAAAAAA	290
RESULT 182			
A1073068/c			
LOCUS	A1073068	312 bp	mRNA
DEFINITION	UT-R-YO-1Y-C-02-0-U-II	UT-R-YO	Rattus norvegicus cDNA clone
	UT-R-YO-1Y-C-02-0-U-II	mRNA sequence	
		EST	11-FEB-1999

ACCESSION A1073068
KEYWORDS EST
GI:339362
SOURCE Norway rat.
ORGANISM Rattus norvegicus
TISSUE Adipocytes; Chondria; Cranialia; Ventricle; Endothelium;
Fat; Kidney; Liver; Muscle; Pancreas; Skin; Spleen; Testis;
Tissue; Uterine; Blood; Bone; Brain; Cardiac; Colon; Esophagus;
Heart; Intestine; Kidney; Liver; Lung; Muscle; Nerve;
Pancreas; Skin; Spleen; Stomach; Thymus; Tumor; Uterus;
Whole Body
REFERENCE 1 (bases 1 to 313)
AUTHORS Bonaldi,M.F., Lamm,G. and Soares,M.B.
JOURNAL Genomics
COMMENT Normalization and subtraction: two approaches to facilitate gene
expression analysis
CONTACT Soares, MB
Genome Res. 6 (7), 791-806 (1996)
9704447

University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel.: 319 335 9755
Fax: 319 335 9758
Email: macaestabine-weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
oligo of 12bp served to identify it as a clone from the normalised
adult C56/J library. cDNA library Preparation, N. Irlbaum (unpublished
data). The distribution of clones will be available through Research
Genetics.
Seq primer: M3 Forward.
Location/Qualifiers
1..3118+name="ratara.norvegicus"
/db_xref="taxon:10116"
/db_xref="taxon:10116"
/clone="U1-R-Y0-1x-4-02-0-01"
/clone="11b-U1-R-Y0"
/db_xref="taxon:10116"
/lab_host="CHN08 (Life Technologies)"

polymerase (Pfu) (BioLabs, Beverly, MA). The *Utr-R* library is a subtracted library derived from an individually-sieved normalized whole-eye (minus the lens) library. The driver for the subtraction consisted of a pool of all previous libraries (*Utr-R1*, *Utr-R2*, *Utr-R3*, *Utr-R4*, *Utr-R5*, *Utr-R6*, *Utr-R7*, *Utr-R8*, *Utr-R9*, *Utr-R10*, *Utr-R11*, *Utr-R12*, *Utr-R13*, *Utr-R14*, *Utr-R15*, *Utr-R16*, *Utr-R17*, *Utr-R18*, *Utr-R19*, *Utr-R20*, *Utr-R21*, *Utr-R22*, *Utr-R23*, *Utr-R24*, *Utr-R25*, *Utr-R26*, *Utr-R27*, *Utr-R28*, *Utr-R29*, *Utr-R30*, *Utr-R31*, *Utr-R32*, *Utr-R33*, *Utr-R34*, *Utr-R35*, *Utr-R36*, *Utr-R37*, *Utr-R38*, *Utr-R39*, *Utr-R40*, *Utr-R41*, *Utr-R42*, *Utr-R43*, *Utr-R44*, *Utr-R45*, *Utr-R46*, *Utr-R47*, *Utr-R48*, *Utr-R49*, *Utr-R50*, *Utr-R51*, *Utr-R52*, *Utr-R53*, *Utr-R54*, *Utr-R55*, *Utr-R56*, *Utr-R57*, *Utr-R58*, *Utr-R59*, *Utr-R60*, *Utr-R61*, *Utr-R62*, *Utr-R63*, *Utr-R64*, *Utr-R65*, *Utr-R66*, *Utr-R67*, *Utr-R68*, *Utr-R69*, *Utr-R70*, *Utr-R71*, *Utr-R72*, *Utr-R73*, *Utr-R74*, *Utr-R75*, *Utr-R76*, *Utr-R77*, *Utr-R78*, *Utr-R79*, *Utr-R80*, *Utr-R81*, *Utr-R82*, *Utr-R83*, *Utr-R84*, *Utr-R85*, *Utr-R86*, *Utr-R87*, *Utr-R88*, *Utr-R89*, *Utr-R90*, *Utr-R91*, *Utr-R92*, *Utr-R93*, *Utr-R94*, *Utr-R95*, *Utr-R96*, *Utr-R97*, *Utr-R98*, *Utr-R99*, *Utr-R100*, *Utr-R101*, *Utr-R102*, *Utr-R103*, *Utr-R104*, *Utr-R105*, *Utr-R106*, *Utr-R107*, *Utr-R108*, *Utr-R109*, *Utr-R110*, *Utr-R111*, *Utr-R112*, *Utr-R113*, *Utr-R114*, *Utr-R115*, *Utr-R116*, *Utr-R117*, *Utr-R118*, *Utr-R119*, *Utr-R120*, *Utr-R121*, *Utr-R122*, *Utr-R123*, *Utr-R124*, *Utr-R125*, *Utr-R126*, *Utr-R127*, *Utr-R128*, *Utr-R129*, *Utr-R130*, *Utr-R131*, *Utr-R132*, *Utr-R133*, *Utr-R134*, *Utr-R135*, *Utr-R136*, *Utr-R137*, *Utr-R138*, *Utr-R139*, *Utr-R140*, *Utr-R141*, *Utr-R142*, *Utr-R143*, *Utr-R144*, *Utr-R145*, *Utr-R146*, *Utr-R147*, *Utr-R148*, *Utr-R149*, *Utr-R150*, *Utr-R151*, *Utr-R152*, *Utr-R153*, *Utr-R154*, *Utr-R155*, *Utr-R156*, *Utr-R157*, *Utr-R158*, *Utr-R159*, *Utr-R160*, *Utr-R161*, *Utr-R162*, *Utr-R163*, *Utr-R164*, *Utr-R165*, *Utr-R166*, *Utr-R167*, *Utr-R168*, *Utr-R169*, *Utr-R170*, *Utr-R171*, *Utr-R172*, *Utr-R173*, *Utr-R174*, *Utr-R175*, *Utr-R176*, *Utr-R177*, *Utr-R178*, *Utr-R179*, *Utr-R180*, *Utr-R181*, *Utr-R182*, *Utr-R183*, *Utr-R184*, *Utr-R185*, *Utr-R186*, *Utr-R187*, *Utr-R188*, *Utr-R189*, *Utr-R190*, *Utr-R191*, *Utr-R192*, *Utr-R193*, *Utr-R194*, *Utr-R195*, *Utr-R196*, *Utr-R197*, *Utr-R198*, *Utr-R199*, *Utr-R200*, *Utr-R201*, *Utr-R202*, *Utr-R203*, *Utr-R204*, *Utr-R205*, *Utr-R206*, *Utr-R207*, *Utr-R208*, *Utr-R209*, *Utr-R210*, *Utr-R211*, *Utr-R212*, *Utr-R213*, *Utr-R214*, *Utr-R215*, *Utr-R216*, *Utr-R217*, *Utr-R218*, *Utr-R219*, *Utr-R220*, *Utr-R221*, *Utr-R222*, *Utr-R223*, *Utr-R224*, *Utr-R225*, *Utr-R226*, *Utr-R227*, *Utr-R228*, *Utr-R229*, *Utr-R230*, *Utr-R231*, *Utr-R232*, *Utr-R233*, *Utr-R234*, *Utr-R235*, *Utr-R236*, *Utr-R237*, *Utr-R238*, *Utr-R239*, *Utr-R240*, *Utr-R241*, *Utr-R242*, *Utr-R243*, *Utr-R244*, *Utr-R245*, *Utr-R246*, *Utr-R247*, *Utr-R248*, *Utr-R249*, *Utr-R250*, *Utr-R251*, *Utr-R252*, *Utr-R253*, *Utr-R254*, *Utr-R255*, *Utr-R256*, *Utr-R257*, *Utr-R258*, *Utr-R259*, *Utr-R260*, *Utr-R261*, *Utr-R262*, *Utr-R263*, *Utr-R264*, *Utr-R265*, *Utr-R266*, *Utr-R267*, *Utr-R268*, *Utr-R269*, *Utr-R270*, *Utr-R271*, *Utr-R272*, *Utr-R273*, *Utr-R274*, *Utr-R275*, *Utr-R276*, *Utr-R277*, *Utr-R278*, *Utr-R279*, *Utr-R280*, *Utr-R281*, *Utr-R282*, *Utr-R283*, *Utr-R284*, *Utr-R285*, *Utr-R286*, *Utr-R287*, *Utr-R288*, *Utr-R289*, *Utr-R290*, *Utr-R291*, *Utr-R292*, *Utr-R293*, *Utr-R294*, *Utr-R295*, *Utr-R296*, *Utr-R297*, *Utr-R298*, *Utr-R299*, *Utr-R300*, *Utr-R301*, *Utr-R302*, *Utr-R303*, *Utr-R304*, *Utr-R305*, *Utr-R306*, *Utr-R307*, *Utr-R308*, *Utr-R309*, *Utr-R310*, *Utr-R311*, *Utr-R312*, *Utr-R313*, *Utr-R314*, *Utr-R315*, *Utr-R316*, *Utr-R317*, *Utr-R318*, *Utr-R319*, *Utr-R320*, *Utr-R321*, *Utr-R322*, *Utr-R323*, *Utr-R324*, *Utr-R325*, *Utr-R326*, *Utr-R327*, *Utr-R328*, *Utr-R329*, *Utr-R330*, *Utr-R331*, *Utr-R332*, *Utr-R333*, *Utr-R334*, *Utr-R335*, *Utr-R336*, *Utr-R337*, *Utr-R338*, *Utr-R339*, *Utr-R340*, *Utr-R341*, *Utr-R342*, *Utr-R343*, *Utr-R344*, *Utr-R345*, <

3-5 nucleotides present between the Not I site and the 1019bp of track which allows identification of the library (UTR-RV) was constructed as follows: PCR amplified cDNA inserts from previous library clones from which 3' ESTs had been derived were used as a diver in the PCR reaction with the normalized whole-eye library in single-stranded cDNA (subcloned library) was purified by hydroxyapatite column chromatography, converted to double-stranded cDNAs and electroporated into DH10B library. This procedure has been previously described (Bonaldi, Lannon and Soares, Genome Research 6: 791-806, 1996).

77 a 196b 70 c 66 g 99 c

BASE COUNT
ORIGIN

Query Match
Read Location
Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0

0y 383 tttatgaaataaaaaaaa 402
Db 23 tttatgaaataaaaaaaa 4

Result 183
AW76811.c
LOCUS AW76811.c
DEFINITION
accession
version
keywords
organism
source
cdd
comment

AW76811.1 314 bp mRNA
n151309.gb NCI/CCG/CCL4 Homo sapiens cDNA clone IMAGE:3004937 3'
hm151309.xb NCI/6069 ELONGATION FACTOR 1-ALPHA 1 (HUMAN); mRNA
AW76811.1
AW76811.1 GI:7700835
EST

Homo sapiens
Human
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Chromosome Microarray Project (CGAP),
Bamert-Buck, M.D., Ph.D., Michael R.

04-MAY-2000
IMAGE:3004937 3'

[illegible][illegible]

```

Nov 27 09:13:21 2001                                uu-410-835-a.01lg.txt

GAGACAGACAGCCGCCGCACATCGACATCTTTTTCCTTTTTTTTTCN 3]. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length b
cDNA after second strand cDNA was prepared with the
GAGACAGACATCTCCCACTTAAATTATTAATACCCCCTCCCCC 3'}. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda PLo 1.*

BLAST COUNT                                           63      83 c      72 g      96 t

ORIGIN
Query Match          0 3%. Score 20; DB 132; Length 114;
Best Local Similarity: 100.0%; Pied No. 2,2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy       75 |ttcttccacattggttc| 94
Db        258 |TTTCTTTCACATTTTGTC| 277

RESULT 185
AN265414/c
LOCUS
DISCUSSION
DESCRIPTION
similar to gb:U08471 (trial protein-CUTRININ)
GAMMA-GUTTERALTRANSFERRIN K (HUMAN); mRNA sequence.
Accession
AN265414
VERSION 1
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eumetazoa; Platyrrhini; Primates; Caeartaria; Hominoidea; Homo.
NCBI COAR Blast://www.ncbi.nlm.nih.gov/coarblast.

```

```

/organism="Mus musculus"
/clone="D63002J11"
/clone_1db=Riken full-length enriched, 0 day neonate
kidney"
/tissue_type="kidney"
/age="postnatal 0 day neonate"
/lab_host="DH10B"
/notes="Site 1: Sal1; Site 2: BamHI. cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
project of Genome Exploration Research Group in Riken
IRID. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer 15

```

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL *Computational Biology* (1997)
COMMENTS Comput Biol Bioinform. Ph. D.
Cottrell, R. S. Strausberg, Ph. D.
Tel.: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Edward Shtiliec Ph.D., Silvio Gutkind Ph.D.,
Michael Schreiber Ph.D., David Baltimore Ph.D.,
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CGAP Library Preparation: David Baltimore Ph.D.
CGAP DNA Sequencing by: Washington University Genome Sequencing Center
CGAP Data Distribution: NIH-CCAP clone distribution information can be
found at: <http://www.ncbi.nlm.nih.gov/ibdb/cgap/clone.html>
Seq primer: -400P from Gibco.

FEATURES

3-1-1 Toyoda, Tawhuwa, Ibexaki 305-0074, Japan
Tel.: +81-298-36-9013
Email: genome@rtc.riken.go.jp/
Utl.NtUp//genome.rtc.riken.go.jp/,
Genomic.P., Nishiyama.Y., Motoyoshi.A., Itoh.M., Ozakiki.T., Muramatsu.M. and Hayashizaki.Y.
RNA interference as a tool for identifying essential genes by
tetrazole and its application for the synthesis of full length
cDNA. Proc. Natl Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh.M., Kitamura.Y., Aikawa.J., Shibata.Y., Izawa.H., Ozakiki.T.,
Motoyoshi.A. and Hayashizaki.Y., Shibata.Y., Osada,T., Muramatsu,M., Kawachi.M., Nakai.K.

Automated filter-tip-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

Please visit our web site (<http://genome rtc.riken go jp>) for
further details.

COMMENTS

[illegible]

TYPE Mar 27 09:32:21 2001

us-09-410-835-4.011g.rst

Page 267

```

BASE COUNT          74      g c t a        80 t
ORIGIN
Query Match              0.39   Score 20; DB No. Length 319;
Best Local Similarity 100.0%; Pctd. No. 2,2e+02;
Matches    20; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
QY         363 ttatgttttgggagaaataaaa 402
                |||||||
Db          20 TTATGTTTTTAAAAA       1

REFERENCE 1 A17510B5     .j19 bp mRNA EST 22-NOV-1999
DEFINITION CRJ0H02.XZ J1a Bone marrow stroma Homo sapiens CDNA clone
ACCESSION A17510B5
VERSION A17510B5
KEYWORDS EST.
SOURCE Human, Spleen
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euarchonta; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 319) Touchman, J.W., Bouffard, G.G.,
ADDITION Beckerator-Streiberg, S.M., Green, E.D.,
AUTHORS P.C.G., Hochstim, R.N., and Pandemonio, C.A.
TITLE SCAR: The Swissrat Genome Anatomy Project
COMMENT Genbank submission ID# U08053
NATIONAL MEDICAL GENETICS BRANCH
National Human Genome Research Institute
10/OTC01, 9000 Rockville Pike, Bethesda, MD 20892-1257, USA
Fax: 301-496-7157
Email: libidn@nih.nih.gov
DNA Sequencing and analyses by National Institutes of Health
Genetic Engineering Center (NIHC).
Pictet et al. (1993)
Seq primer: 2'HK3 forward primer (ABF).
FEATURES             1..319
Source               Location/Organisms
```

```

Db          241   ATTTGACAAAGAGCAATGAAAAA 222
Query Match      0.31; Score 20; Db 98; Length 318;
Best Local Statistic 100.0%; Pred. No. 2.2e+02;
Mismatches    0; Mismatches    0; Indels    0; Gaps    0
OY           382   attatcggataaaaaaaaaaa 401
RESULT 169
LOCUS 617/c
DEFINITION
ACCESSION
VERSION
KEYWORDS
ORGNAMSK
human
human sapiens
Chordates; Chordata; Chnitiia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo
NCBI-GAP http://www.ncbi.nlm.nih.gov/mgap;
1 (bases 1 to 319)
AUTHORS
Unpublished (1997)
JOURNAL
CONTACT: Robert Strumberg, Ph.D.
Email: robert.strumberg@nih.gov
Title
Number Gene Index
Tissue Procurement: Christopher Koskuluik, M.D., Ph.D., Michael R. Emery-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by Washington University Genome Sequencing Center
Clone distribution: NCI-CoAP clone distribution information can be
found through the I.M.A.C.B. Consortium/LNLB at:
Seq primer: -dGMP from CldU-Image.html
High quality sequence atop .jii.
FEATURES
source
location/Qualifiers
1..organs=Homo sapiens*
/db_xref=taxon:9606*
/clone=IMAGE:2136956*
/gene=ITID=NCI-CoAP_Kid11*
/name=Organ: kidney; Vector: pETTD-Pac (Pharmacia) with
a modified polylinker; Site:1: Not I; Site-2: Eco RI;
Plasmid DNA from the normalized library NCI-CoAP_kid3 was

```

[illegible]

BASE COUNT 117 a 36 c 64 g 113 t
ORIGIN

Query Match 0.31: Score 20: DB 141: Length 330:
Best Local Similarity 100.00: Pred No. 2 2c102:
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 5026 ttgcctttaaattttatc 5045
|||||
Db 146 ttgcctttaaattttatt 165

Search completed: March 26, 2001, 17:53:03
Job time: 20232 sec

c 976 16 0.3 4699 1 US-08-487-890A-1 Sequence 1, Appl
 c 977 16 0.3 4699 2 US-08-476-435-1 Sequence 1, Appl
 c 978 16 0.3 4699 3 US-08-435-435-1 Sequence 1, Appl
 c 979 16 0.3 4699 4 US-08-435-435-1 Sequence 1, Appl
 c 980 16 0.3 4699 5 US-08-435-435-1 Sequence 1, Appl
 c 981 16 0.3 4699 6 US-08-435-435-1 Sequence 1, Appl
 c 982 16 0.3 4699 7 US-08-435-435-1 Sequence 1, Appl
 c 983 16 0.3 4699 8 US-08-435-435-1 Sequence 1, Appl
 c 984 16 0.3 4699 9 US-08-435-435-1 Sequence 1, Appl
 c 985 16 0.3 4699 10 US-08-435-435-1 Sequence 1, Appl
 c 986 16 0.3 4699 11 US-08-435-435-1 Sequence 1, Appl
 c 987 16 0.3 4699 12 US-08-435-435-1 Sequence 1, Appl
 c 988 16 0.3 4699 13 US-08-435-435-1 Sequence 1, Appl
 c 989 16 0.3 4699 14 US-08-435-435-1 Sequence 1, Appl
 c 990 16 0.3 4699 15 US-08-435-435-1 Sequence 1, Appl
 c 991 16 0.3 4699 16 US-08-435-435-1 Sequence 1, Appl
 c 992 16 0.3 4699 17 US-08-435-435-1 Sequence 1, Appl
 c 993 16 0.3 4699 18 US-08-435-435-1 Sequence 1, Appl
 c 994 16 0.3 4699 19 US-08-435-435-1 Sequence 1, Appl
 c 995 16 0.3 4699 20 US-08-435-435-1 Sequence 1, Appl
 c 996 16 0.3 4699 21 US-08-435-435-1 Sequence 1, Appl
 c 997 16 0.3 4699 22 US-08-435-435-1 Sequence 1, Appl
 c 998 16 0.3 4699 23 US-08-435-435-1 Sequence 1, Appl
 c 999 16 0.3 4699 24 US-08-435-435-1 Sequence 1, Appl
 c 1000 16 0.3 4699 25 US-08-435-435-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
 US-08-470-260-4
 GENERAL INFORMATION:
 PATENT NO. 6,077,706
 APPLICANT: Covacell, Antennalio
 APPLICANT: Biogen, Inc.
 APPLICANT: Macchia, Giovanni
 APPLICANT: Rappelli, Rino
 TITLE OF INVENTION: Helicobacter Pylori Protein Useful
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESS: Chilton Corporation
 STREET: 4500 Horton Street
 CITY: San Diego, CA
 STATE: California
 COUNTRY: USA
 ZIP: 94508-2916
 COMPUTER READABLE FORM:

c 976 16 0.3 4699 1 US-08-487-890A-1 Sequence 1, Appl
 c 977 16 0.3 4699 2 US-08-476-435-1 Sequence 1, Appl
 c 978 16 0.3 4699 3 US-08-435-435-1 Sequence 1, Appl
 c 979 16 0.3 4699 4 US-08-435-435-1 Sequence 1, Appl
 c 980 16 0.3 4699 5 US-08-435-435-1 Sequence 1, Appl
 c 981 16 0.3 4699 6 US-08-435-435-1 Sequence 1, Appl
 c 982 16 0.3 4699 7 US-08-435-435-1 Sequence 1, Appl
 c 983 16 0.3 4699 8 US-08-435-435-1 Sequence 1, Appl
 c 984 16 0.3 4699 9 US-08-435-435-1 Sequence 1, Appl
 c 985 16 0.3 4699 10 US-08-435-435-1 Sequence 1, Appl
 c 986 16 0.3 4699 11 US-08-435-435-1 Sequence 1, Appl
 c 987 16 0.3 4699 12 US-08-435-435-1 Sequence 1, Appl
 c 988 16 0.3 4699 13 US-08-435-435-1 Sequence 1, Appl
 c 989 16 0.3 4699 14 US-08-435-435-1 Sequence 1, Appl
 c 990 16 0.3 4699 15 US-08-435-435-1 Sequence 1, Appl
 c 991 16 0.3 4699 16 US-08-435-435-1 Sequence 1, Appl
 c 992 16 0.3 4699 17 US-08-435-435-1 Sequence 1, Appl
 c 993 16 0.3 4699 18 US-08-435-435-1 Sequence 1, Appl
 c 994 16 0.3 4699 19 US-08-435-435-1 Sequence 1, Appl
 c 995 16 0.3 4699 20 US-08-435-435-1 Sequence 1, Appl
 c 996 16 0.3 4699 21 US-08-435-435-1 Sequence 1, Appl
 c 997 16 0.3 4699 22 US-08-435-435-1 Sequence 1, Appl
 c 998 16 0.3 4699 23 US-08-435-435-1 Sequence 1, Appl
 c 999 16 0.3 4699 24 US-08-435-435-1 Sequence 1, Appl
 c 1000 16 0.3 4699 25 US-08-435-435-1 Sequence 1, Appl

QUERY MATCH 100.0% Score 5925; DB 3; Length 5925;
 Matches 5925; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE: 5925 Nucleic acid
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULAR WEIGHT: 10000
 CYPOTYPE: linear
 WOTYPE: DNA (genomic)

c 976 16 0.3 4699 1 US-08-487-890A-1 Sequence 1, Appl
 c 977 16 0.3 4699 2 US-08-476-435-1 Sequence 1, Appl
 c 978 16 0.3 4699 3 US-08-435-435-1 Sequence 1, Appl
 c 979 16 0.3 4699 4 US-08-435-435-1 Sequence 1, Appl
 c 980 16 0.3 4699 5 US-08-435-435-1 Sequence 1, Appl
 c 981 16 0.3 4699 6 US-08-435-435-1 Sequence 1, Appl
 c 982 16 0.3 4699 7 US-08-435-435-1 Sequence 1, Appl
 c 983 16 0.3 4699 8 US-08-435-435-1 Sequence 1, Appl
 c 984 16 0.3 4699 9 US-08-435-435-1 Sequence 1, Appl
 c 985 16 0.3 4699 10 US-08-435-435-1 Sequence 1, Appl
 c 986 16 0.3 4699 11 US-08-435-435-1 Sequence 1, Appl
 c 987 16 0.3 4699 12 US-08-435-435-1 Sequence 1, Appl
 c 988 16 0.3 4699 13 US-08-435-435-1 Sequence 1, Appl
 c 989 16 0.3 4699 14 US-08-435-435-1 Sequence 1, Appl
 c 990 16 0.3 4699 15 US-08-435-435-1 Sequence 1, Appl
 c 991 16 0.3 4699 16 US-08-435-435-1 Sequence 1, Appl
 c 992 16 0.3 4699 17 US-08-435-435-1 Sequence 1, Appl
 c 993 16 0.3 4699 18 US-08-435-435-1 Sequence 1, Appl
 c 994 16 0.3 4699 19 US-08-435-435-1 Sequence 1, Appl
 c 995 16 0.3 4699 20 US-08-435-435-1 Sequence 1, Appl
 c 996 16 0.3 4699 21 US-08-435-435-1 Sequence 1, Appl
 c 997 16 0.3 4699 22 US-08-435-435-1 Sequence 1, Appl
 c 998 16 0.3 4699 23 US-08-435-435-1 Sequence 1, Appl
 c 999 16 0.3 4699 24 US-08-435-435-1 Sequence 1, Appl
 c 1000 16 0.3 4699 25 US-08-435-435-1 Sequence 1, Appl

c 976 16 0.3 4699 1 US-08-487-890A-1 Sequence 1, Appl
 c 977 16 0.3 4699 2 US-08-476-435-1 Sequence 1, Appl
 c 978 16 0.3 4699 3 US-08-435-435-1 Sequence 1, Appl
 c 979 16 0.3 4699 4 US-08-435-435-1 Sequence 1, Appl
 c 980 16 0.3 4699 5 US-08-435-435-1 Sequence 1, Appl
 c 981 16 0.3 4699 6 US-08-435-435-1 Sequence 1, Appl
 c 982 16 0.3 4699 7 US-08-435-435-1 Sequence 1, Appl
 c 983 16 0.3 4699 8 US-08-435-435-1 Sequence 1, Appl
 c 984 16 0.3 4699 9 US-08-435-435-1 Sequence 1, Appl
 c 985 16 0.3 4699 10 US-08-435-435-1 Sequence 1, Appl
 c 986 16 0.3 4699 11 US-08-435-435-1 Sequence 1, Appl
 c 987 16 0.3 4699 12 US-08-435-435-1 Sequence 1, Appl
 c 988 16 0.3 4699 13 US-08-435-435-1 Sequence 1, Appl
 c 989 16 0.3 4699 14 US-08-435-435-1 Sequence 1, Appl
 c 990 16 0.3 4699 15 US-08-435-435-1 Sequence 1, Appl
 c 991 16 0.3 4699 16 US-08-435-435-1 Sequence 1, Appl
 c 992 16 0.3 4699 17 US-08-435-435-1 Sequence 1, Appl
 c 993 16 0.3 4699 18 US-08-435-435-1 Sequence 1, Appl
 c 994 16 0.3 4699 19 US-08-435-435-1 Sequence 1, Appl
 c 995 16 0.3 4699 20 US-08-435-435-1 Sequence 1, Appl
 c 996 16 0.3 4699 21 US-08-435-435-1 Sequence 1, Appl
 c 997 16 0.3 4699 22 US-08-435-435-1 Sequence 1, Appl
 c 998 16 0.3 4699 23 US-08-435-435-1 Sequence 1, Appl
 c 999 16 0.3 4699 24 US-08-435-435-1 Sequence 1, Appl
 c 1000 16 0.3 4699 25 US-08-435-435-1 Sequence 1, Appl

QY	1321	acccttcaattccatccctcggccagcaataggaaatctaaagctctaaagagatcgtctgac	1380
QY	1322	acccttcaattccatccctcggccagcaataggaaatctaaagctctaaagagatcgtctgac	1381
QY	1323	acccttcaattccatccctcggccagcaataggaaatctaaagctctaaagagatcgtctgac	1382
QY	1381	atctaccccaatctctgcatctcaatcaatctgatactgatactcaaacgcgtctctctgac	1440
QY	1382	atctaccccaatctctgcatctcaatcaatctgatactgatactcaaacgcgtctctctgac	1441
QY	1441	ctaatggggagatctatggatagatgaaacggaaatctctctctctgtaagagat	1500
QY	1442	ctaatggggagatctatggatagatgaaacggaaatctctctctctgtaagagat	1501
QY	1501	ggatggcccgctcagagcaatgatctggagacacccgttgctcttaagaacaaataggc	1560
QY	1502	ggatggcccgctcagagcaatgatctggagacacccgttgctcttaagaacaaataggc	1561
QY	1561	acaaagcgcgcgcacaaatctaatgtctctctctgaaacacggagatctgagctctgac	1620
QY	1562	acaaagcgcgcgcacaaatctaatgtctctctctgaaacacggagatctgagctctgac	1621
QY	1621	ggctggcgagaaaggagctctaaaccccgctttctctccctcaaaaaggccactcaaa	1680
QY	1622	ggctggcgagaaaggagctctaaaccccgctttctctccctcaaaaaggccactcaaa	1681
QY	1681	ggccacaaagagctctaaagcacaagaagcgccatccctctctacccctcaaacgcacaa	1740
QY	1682	ggccacaaagagctctaaagcacaagaagcgccatccctctctacccctcaaacgcacaa	1741
QY	1741	ctctcccaaaatctaatctctaaactctgagctggagagaaagagagaaattctgaa	1800
QY	1742	ctctcccaaaatctaatctctaaactctgagctggagagaaagagagaaattctgaa	1801
QY	1801	acgtcaacaaatctaatctctaaactctgagctggagagaaagagagaaattctgaa	1860
QY	1802	acgtcaacaaatctaatctctaaactctgagctggagagaaagagagaaattctgaa	1861
QY	1861	acgtcaacaaatctaatctctaaactctgagctggagagaaagagagaaattctgaa	1920
QY	1862	acgtcaacaaatctaatctctaaactctgagctggagagaaagagagaaattctgaa	1921
QY	1921	acgtcaacaaatctaatctctaaactctgagctggagagaaagagagaaattctgaa	1980
QY	1922	acgtcaacaaatctaatctctaaactctgagctggagagaaagagagaaattctgaa	1981
QY	1981	atggggagaaatgtctatctctcaggatgacctcaaaacacgatacggagctcttgat	2040
QY	1982	atggggagaaatgtctatctctcaggatgacctcaaaacacgatacggagctcttgat	2041
QY	2041	tatctcaattccaatctacccacgctctcccgaaaccccaaaaagggtgtgagccttaag	2100

[illegible]

[illegible][illegible][illegible]

0y 5641 1594AAATCCCAAGGCGTCAAGCAATAGTGTTCGTCGTAAGGTCCTTATATGCA 5700
 Db 1001 TGAAGAAATCAAGGCTGACGCAATCTCTTCATGCTGCTTATGTCGA 1007
 0y 5701 TAAGGAGATCAAGGCTATAGCAATAGTATGTCTCAATATAGGCTTTAA 5760
 Db 1005 TAAAGCATCTGACCGCAACCCCAATAGATATATTCATTAATATTCGCTTTAA 1013
 0y 5761 AAGGCTTTAAAGCGTCAAGCGTCAAGCGCTCAAGGAGCGCTATATGCA 5820
 Db 1015 AAGGCTTTAAAGCGTCAAGCGTCAAGCGCTCAAGGAGCGCTATATGCA 1019
 0y 5821 CTTCTTATTAATAGGATATATAGGATATATAGGATATATAGGATATATAGG 5880
 Db 10195 CTTTATTAATAGGATATATAGGATATATAGGATATATAGGATATATAGG 1023
 0y 5881 TCTCTATCTGCTTATGTATGTATGATATGATATGCAAGCAAGCT 5925
 Db 1035 TCTCTATCTGCTTATGTATGTATGATATGATATGCAAGCAAGCT 10299

 RESULT 6
 US-08-417-451-5/C
 Sequence 5, Application US/08477451
 Patent No. 5928855
 INVENTOR INFORMATION:
 TITLE OF INVENTION: Helicopter Pilot's Cagl Region
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 STREET 4560 Horton Street
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP 94608-2316
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: gnu/gnu, gnu/gnu
 SOFTWARE: Patent Release 11.0, Version 11.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/98/477451
 CLASSIFICATION:
 CLASS NUMBER: G06F 19/00
 ATTORNEY/AGENT INFORMATION:
 NAME: McQuinn, Barbara S.
 REGISTRATION NUMBER: 95,113
 REGISTRATION EXPIRATION DATE: 11/03/2002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 510-601-3708

[illegible]

RESULT 10
US-05-356-437-1
Sequence 1, Application US/09259437
GENERAL INFORMATION:
APPLICANT: COVER, TIMOTHY L.
APPLICANT: BLASER, MARTIN J.
APPLICANT: MANN, KLEATHOUS
APPLICANT: MANN, KLEATHOUS, B.
TITLE OF INVENTION: THE LAM GENE AND METHODS FOR DETECTING
NUMBER OF SEQUENCES: 4
TITLE OF INVENTION: PREDISPOSITION TO PEPTIC ULCERATION AND GASTRIC CANCER
CONVINCING ADDRESS:
ADDRESS: ROSENBERG, P.C.
STREET: 137 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
ZIP: 30309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS/MS-DOS
SOFTWARE: PatentIn Release 11.0, Version 11.25

Tue Mar 27 09:32:18 2001

us-09-410-835-4.011g.rn1

Page 79

RESULT: 1
 1. Sequence 1: Application PC/TUS9109782
 2. GENERAL INFORMATION:
 APPLICANT: COVER, TIMOTHY L.
 APPLICANT: BLASER, MARTIN J.
 APPLICANT: REILLY, JAMES R.
 TITLE OF INVENTION: "THE BLK GENE AND METHODS FOR DETECTING
 TITLE OF INVENTION: PREDISPOSITION TO PEPTIC ULCERATION
 NUMBER OF SEQUENCES: 4
 ADDRESS: POE ADDRESS: ROSENBERG, P. C.
 STREET: 113 Carnegie Way, Suite 400
 CITY: Atlanta
 STATE: Georgia
 ZIP: 30106
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/09782
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: SPRATT, GRENDELIN D.
 REFERENCE NUMBER: 36,010, 009
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404/688-9880
 TELEFAX: 404/688-9880
 INVENTOR INFORMATION:
 SEQUENCE CHARACTERISTICS: 1
 TYPE: nucleic acid
 TOPOLOGY: linear
 LENGTH: 3648 base pairs
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 STRAIN/ISOL: Helicobacter pylori
 NAME/KEY: CDS
 LOCATION: 1072..3648
 CDT-US93-09782-1

Tue Mar 27 09:32:18 2001

us-09-410-635-4.011g.rn1

Page 76

1 CURRENT APPLICATION DATA
2
3 APPLICATION NUMBER: 09/08/259,437
4
5 CLASSIFICATION:
6
7 PRIOR APPLICATION DATA:
8
9 PENDING APPLICATION NUMBER: 09/08/116,397
10
11 PENDING APPLICATION NUMBER:
12
13 ATTORNEY/AGENT INFORMATION:
14
15 NAME: SPATY, GRENDELIN D.
16 FIRM: SPATY, GRENDELIN D.
17 REFERENCE/DOCKET NUMBER: 2,500,030
18 TELEPHONE: 04/688-0770
19 TELEFAX: 04/688-0770
20 INFORMATION FOR SEQ ID NO: 1:
21
22 SEQUENCE CHARACTERISTICS:
23
24 TYPE: nucleic acid
25 STRAND: single
26 STANDARDS: double
27
28 MODIFIERS: linear
29
30 MODIFIED BASES: none (genomic)
31
32 ORIGINAL SOURCE:
33
34 PROBLEM: Helicobacter pylori
35
36 NAME/KEY: CDS
37
38 LOCATION: 1072..1648
39
40 ORIGIN: 09-08-259-437-1

[illegible]

Tue Mar 27 09:32:18 2001

us-09-410-835-4.014g.xml

Page 80

[illegible]

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

[illegible]

Tue Mar 27 09:32:18 2001

us-09-410-035-4.011g.rn1

Page 67

	LENGTH: 4821	base pairs
type:	nucleic acid	
STRANDING:	double	
MOLECULE TYPE:	1 nt	
FEATURE:	DNM (germline)	
NAME/KEY:	CDS	
LOCATION:	1072..4614	
FC7-0593-09182-3		
Query Match	4.0%	Score 235: DB 4: Length 4821:
Best Local Similarity:	99.7%	Pid: No. 8.e-89:
Matches 285:	Conservative	0: Mismatch 1: Indels 0: Gaps 0:
QY 550	ATTACCAACAAACCAACCAACCAACGAGAGCGCGCTTAAACCGACGATTAATCAATATCTT	609
QY 1087	ATTACCAACAAACCAACCAACCAACGAGCGCTTAAACCGACGATTAATCAATATCTT	1146
QY 610	CGATCGCTTCTTAAATCAACAGCGCTTAAACCGACGATTAATCAATATCTT	689
Db 1147	CGATCGCTTCTTAAATCAACAGCGCTTAAACCGCTTAAACCGCTTAAACCGCTTAAACCG	1206
QY 670	ATCGATTGATGAAGAGATAGGATACACAGCAAGCTTTTGAGAGATCGCAATTAAAG	729
Db 1207	ATCGATTGATGAAGAGATAGGATACACAGCAAGCTTTTGAGAGATCGCAATTAAAG	1246
QY 730	GAGAAATCCCAATCAATGAAGAGAGCAAAATCCCTCCACAAAGAGATAGATCTTCCAACT	789
Db 1267	GAGAAATCCCAATCAATGAAGAGAGCAAAATCCCTCCACAAAGAGATAGATCTTTCACAC	1266
QY 790	CTCTCAATCAATGAAGAGAGATCTTCAACCAAGCAATCAATCTTCTCACT	835
Db 1327	CTCTCAATCAATGAAGAGAGATCTTCAACCAAGCAATCAATCTTCTCACT	1372

RESULT 17
 US-08-965-9038-5
 Patent No. 6069225
 SERIAL INFORMATION:
 APPLICANT: NACOTEC, INC.
 TITLE: ANTIMONY, SODIUM, KALCIUM, AND
 ZINC COMPOSITIONS FOR PREVENTING
 TITLE OF INVENTION: PROTEIN AND CODING
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 STREET: 150 Cambridge Ave., Suite 250
 CITY: Palo Alto
 STATE: CA

[illegible]

RESULT 16
 PCT-US93-09782-3
 Sequence 1: Application PCT/US9309782
 Sequence 2: Application PCT/US9309782
 APPLICANT: COVER, TIMOTHY L.
 APPLICANT: BLASER, MARTIN J.
 APPLICANT: TUDHOPE, KUNALI K.R.
 TITLE OF INVENTION: THE TEA GENE AND METHODS FOR DETECTING
 TITLE OF INVENTION: THE TEA GENE AND METHODS FOR DETECTING
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NEEDLE & ROSENBERG, P.C.
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30303
 COMPUTER-READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT INVENTION PRIORITY CLAIMS:
 APPLICATION NUMBER: PCT/US93/09782
 FILING DATE:
 CLASSIFICATION:
 A: COVER, TIMOTHY L.
 NAME/SPRINT INFORMATION:
 REGISTRATION NUMBER: 16,016
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404/566-9880
 TELEFAX: 404/566-9880
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:

Tue Mar 27 09:32:18 2001

us-09-410-835-4.011g.rn1

Page 318

COUNTRY: USA
ZIP: 94106
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: SIMS
SOFTWARE: Patised for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965.903B
FILING DATE: 07-nov-1997
PRIORITY DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/030232
FILING DATE: 07-nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pellibory, Joanne R
FIRM: Pellibory, Joanne R
REFERENCE/DOCKET NUMBER: 1968
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SRD ID NO.: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1604 base pairs
TYPE: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: h-epi1 cDNA
PLASMID:
PARENT/STR: Coding Sequence
LOCATION: 1...417
OTHER INFORMATION:
US-08-965-903B-5

```

QY      392      attcagcaaaaaaaaaaaaaa 402
Db      1580      attcagcaaaaaaaaaaaaaa 1600

Query Match      0.44; Score 21; DB 3; Length 1604;
Mismatch 1; Gap 0; Identity 100.0%;
Mismatch 0; Conservative 0; Indels 0; Gaps 0;
Mechanics 0;

RESULT 18
US 2002/0108642
Sequence 6 Application US/09012198
Patent No. 6134971

```

GENERAL INFORMATION:
APPLICANT: P.L. Iversen, et al.
TITLE OF INVENTION: Method and Conjugate for Treating
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
CITY: 15000 Lindridge Ave. 560-250
STATE: Palo Alto
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS Compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/02/198
APPLICATION NUMBER: 05/09/02/198
FILING DATE: 23-JAN-1998
CLASSIFICATION: 514
PRIORITY DATA:
APPLICATION NUMBER: 08/848,844
FILING DATE: 30-APR-1997
PRIOR APPLICATION DATA: 60/036,366
APPLICATION NUMBER: 60/036,366
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dehlinger, Peter J
REGISTRATION NUMBER: 28006
REFERENCE/DOC# NUMBER: 59042/SEE 36525/US/A
TELEPHONE: 650 324-0880
TELEFAX: 650 324-0880
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-013-198-6

Tue Mar 27 09:32:18 2001

us-09-410-835-4.o11g.rml

Page 91

Query Match
Database Similarity: 100.0%; Pred. No. 29;
Matches: 20; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
QY 5316 gaataataacagatcagag 5335
DB 2 GAAATATATACGATCAGAG 21
RESULT 20
US-08-377-192-50
Sequence 50: Application US/08/77/192
Patent No. 5924669
GENERAL INFORMATION:
APPLICANT: BROGAERT, WILLEM F.
APPLICANT: CAMORE, BRUNO P.A.
APPLICANT: OSBORN, ROBERT H.
APPLICANT: REES, SARAH B.
APPLICANT: TERBAS, FRANKY R.G.
APPLICANT: VANDERLEIDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/77/192
APPLICATION NUMBER: 08/08/77/192
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KORULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOC# NUMBER: 59042/SEE 36525/US/A
TELEPHONE: 202-861-3000
TELEFAX: 202-821-0944
INFORMATION FOR SEQ ID NO: 50:

Tue Mar 27 09:32:18 2001

us-09-410-835-4.o11g.rml

Page 90

RESULT 19
US-08-377-687-50
Sequence 50: Application US/08/37/687
Patent No. 5586325
GENERAL INFORMATION:
APPLICANT: BROGAERT, WILLEM F.
APPLICANT: CAMORE, BRUNO P.A.
APPLICANT: OSBORN, ROBERT H.
APPLICANT: REES, SARAH B.
APPLICANT: TERBAS, FRANKY R.G.
APPLICANT: VANDERLEIDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/37/687
APPLICATION NUMBER: 08/08/37/687
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KORULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOC# NUMBER: 59042/SEE 36525/US/A
TELEPHONE: 202-861-3000
TELEFAX: 202-821-0944
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 bases
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLTYPE: CDNA
NAME/KEY: CDG
LOCATION: 1..108
US-08-377-687-50

Tue Mar 27 09:32:18 2001

us-09-410-835-4.o11g.rml

Page 92

SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLTYPE: CDNA
NAME/KEY: CDG
LOCATION: 1..108
US-08-377-192-50
Query Match
Database Similarity: 100.0%; Pred. No. 24;
Matches: 20; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
QY 5316 gaataataacagatcagag 5335
DB 2 GAAATATATACGATCAGAG 21
RESULT 21
US-08-839-008-1
Sequence 1: Application US/08/83/008
Patent No. 5918788
GENERAL INFORMATION:
APPLICANT: BAILE, MARK R.
APPLICANT: MCDONNELL, PETER C.
APPLICANT: MCNULTY, DEAN E.
APPLICANT: ROSEN, CRAIG A.
APPLICANT: SHERMAN, JAMES D.
APPLICANT: YOUNG, PETER R.
TITLE OF INVENTION: Smooth Muscle Cell-Derived Migration Factor
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/83/008
APPLICATION NUMBER: 08/08/83/008
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/563,697
FILING DATE: 28-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAUMGARTNER, KATH
REGISTRATION NUMBER: 18,813
TELEPHONE: 610-270-5096
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5096
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1537 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-839-008-1

Query Match 0.34: Score 20: DB 2: Length 1537:
Best Local Similarity 100.0%: Pred. No. 21:
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 1505 TTATGCAAAAAAAAAAAAAA 1524

RESULT 22
US-08-036-210-6
Sequence 6, Application US/08036210
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
INVENTOR: Moller, Karin B.
TITLE OF INVENTION: A NOVEL PROTEIN TYROSINE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: PENNIE & EDWARDS
CITY: New York
STATE: New York
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

STATE: New York
COUNTRY: U.S.A.
ZIP: 10016-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449 609
CLASSIFICATION: 435-1595
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/036 210
INVENTOR: Moller, Niels P.H.
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
TELEPHONE: 212-790-9090
TELEFAX: 212-669-8864/9741
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2173 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1830
OTHER INFORMATION: /note="N=unknown nucleotide"
US-08-449-609-6

Query Match 0.34: Score 20: DB 2: Length 2173:
Best Local Similarity 100.0%: Pred. No. 21:
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 2338 TTATGCAAAAAAAAAAAAAA 2157

RESULT 22
US-08-036-210-10
Sequence 10, Application US/08036210
Patent No. 5583733
GENERAL INFORMATION:

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/036 210
FILING DATE: 23-MAR-1993
CLASSIFICATION: 435-1595
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
TELEPHONE: 212-790-9090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-669-8864/9741
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2173 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1830
OTHER INFORMATION: /note="N=unknown nucleotide"
US-08-036-210-6

Query Match 0.34: Score 20: DB 1: Length 2173:
Best Local Similarity 100.0%: Pred. No. 21:
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 2118 TTATGCAAAAAAAAAAAAAA 2157

RESULT 23
US-08-449-609-6
Sequence 6, Application US/08449609
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
INVENTOR: Moller, Karin B.
TITLE OF INVENTION: A NOVEL PROTEIN TYROSINE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: PENNIE & EDWARDS
CITY: New York
STATE: New York
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036 210
INVENTOR: Moller, Niels P.H.
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
TELEPHONE: 212-790-9090
TELEFAX: 212-669-8864/9741
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2109 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1830
OTHER INFORMATION: /note="N=unknown nucleotide"
US-08-036-210-10

APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
INVENTOR: Moller, Karin B.
TITLE OF INVENTION: A NOVEL PROTEIN TYROSINE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: PENNIE & EDWARDS
CITY: New York
STATE: New York
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036 210
INVENTOR: Moller, Niels P.H.
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
TELEPHONE: 212-790-9090
TELEFAX: 212-669-8864/9741
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2109 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1830
OTHER INFORMATION: /note="N=unknown nucleotide"
US-08-036-210-10

Query Match 0.34: Score 20: DB 1: Length 2109:
Best Local Similarity 100.0%: Pred. No. 21:
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 2274 TTATGCAAAAAAAAAAAAAA 2293

RESULT 23
US-08-036-210-10
Sequence 10, Application US/08036210
Patent No. 5583733
GENERAL INFORMATION:

RESULT 25
US-08-449-609-10
Sequence 10: Application US/08449609
Patent No. 5952212
GENERAL INFORMATION: Nilsa P. H.
APPLICANT: Moller, Ralf B.
TITLE OF INVENTION: TGF- β 1: A NOVEL PROTEIN TYROSINE
KINASE
ADDRESS: 1155 Avenue of the Americas
STATE: New York
CITY: New York
COUNTRY: U.S.A.
ZIP: 10016-2711
COMPUTER READABLE FORM: 414
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 435
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA: US 09/036,210
APPLICATION NUMBER: 09/036,210
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
TELEPHONE: 212-790-9090
TELEFAX: 212-669-8864/9741
INFORMATION: 10
LENGTH: 2309 base pairs
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
MOLCULE TYPE: double
FEATURE:
NAME/KEY: misc_feature
LOCATION: 116
OTHER INFORMATION: /note="X=unknown nucleotide"

Tue Mar 27 09:32:18 2001

us-09-410-835-4.011g.rml

Page 99

ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGIN/L SOURCE: Transforming Growth Factor-Beta 3
IMMEDIATE SOURCE: TGF- β 3
FEATURE:
NAME/KEY: CDS 1498
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 363..1498
OTHER INFORMATION:
PCT-US91-04541.1

Query Match 0.3% Score 20; DB 4; Length 2529;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 389 aaaaaaaaaaaaaaaaaaagctg 408
Db 1981 aaaaaaaaaaaaaaaaaaagctg 1962

RESULT 27
US-08-449-609-10
Sequence 10: Application US/08449609
Patent No. 5952212
GENERAL INFORMATION: Nilsa P. H.
APPLICANT: Moller, Ralf B.
TITLE OF INVENTION: TGF- β 1: A NOVEL PROTEIN TYROSINE
KINASE
ADDRESS: 1155 Avenue of the Americas
STATE: New York
CITY: New York
COUNTRY: U.S.A.
ZIP: 10016-2711
COMPUTER READABLE FORM: 414
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 435
PRIORITY APPLICATION DATA: US 09/036,210
APPLICATION NUMBER: 09/036,210
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
TELEPHONE: 212-790-9090
TELEFAX: 212-669-8864/9741
INFORMATION: 10
LENGTH: 2309 base pairs
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
MOLCULE TYPE: double
FEATURE:
NAME/KEY: misc_feature
LOCATION: 116
OTHER INFORMATION: /note="X=unknown nucleotide"

Tue Mar 27 09:32:18 2001

us-09-410-835-4.011g.rml

Page 98

US-08-449-609-10
Query Match 0.3% Score 20; DB 2; Length 2309;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 383 aaaaaaaaaaaaaaaaaaagctg 402
Db 2274 aaaaaaaaaaaaaaaaaaagctg 2293
RESULT 26
PCT-US91-04541-1/C
Sequence 10: Application PC/T09104541
GENERAL INFORMATION: Oncogene Science Inc.
APPLICANT: Moller, Ralf B.
TITLE OF INVENTION: TGF- β 1: A NOVEL PROTEIN TYROSINE
KINASE
ADDRESS: 1155 Avenue of the Americas
STATE: New York
CITY: New York
COUNTRY: U.S.A.
ZIP: 10016-2711
COMPUTER READABLE FORM: 414
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA: 435
PRIORITY APPLICATION DATA: US 09/036,210
APPLICATION NUMBER: 09/036,210
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
TELEPHONE: 212-790-9090
TELEFAX: 212-669-8864/9741
INFORMATION: 10
LENGTH: 2309 base pairs
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
MOLCULE TYPE: double
FEATURE:
NAME/KEY: misc_feature
LOCATION: 116
OTHER INFORMATION: /note="X=unknown nucleotide"

Tue Mar 27 09:32:18 2001

us-09-410-835-4.011g.rml

Page 100

US-08-449-609-10
Query Match 0.3% Score 20; DB 5; Length 2529;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 389 aaaaaaaaaaaaaaaaaaagctg 408
Db 1981 aaaaaaaaaaaaaaaaaaagctg 1962

RESULT 28
US-08-449-609-10
Sequence 10: Application US/08449609
Patent No. 5952212
GENERAL INFORMATION: Nilsa P. H.
APPLICANT: Moller, Ralf B.
TITLE OF INVENTION: TGF- β 1: A NOVEL PROTEIN TYROSINE
KINASE
ADDRESS: 1155 Avenue of the Americas
STATE: New York
CITY: New York
COUNTRY: U.S.A.
ZIP: 10016-2711
COMPUTER READABLE FORM: 414
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 435
PRIORITY APPLICATION DATA: US 09/036,210
APPLICATION NUMBER: 09/036,210
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
TELEPHONE: 212-790-9090
TELEFAX: 212-669-8864/9741
INFORMATION: 10
LENGTH: 2309 base pairs
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
MOLCULE TYPE: double
FEATURE:
NAME/KEY: misc_feature
LOCATION: 116
OTHER INFORMATION: /note="X=unknown nucleotide"

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
NAME/KEY: m145-feature
LOCATION: 2149
OTHER INFORMATION: /note= "N=unknown nucleotide"

Query Match 0.31: Score 20; DB 1; Length 2692;
Best Local Similarity 100.0%; Pred. No. 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 2657 TTTATCAAAAAAAAAAAAAA 2676
|||||

RESULT 29
US-08-449-609-14
Sequence 14: Application US/08449609
Patent No. 5952112

GENERAL INFORMATION:
APPLICANT: Molter, Niels P.H.
INVENTOR: Molter, Niels P.H.
TITLE OF INVENTION: PTP-511: A NOVEL PROTEIN TYROSINE
KINASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
EIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIORITY INFORMATION:
PRIOR APPLICATION NUMBER: US 08/036,210
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:

Tue Mar 27 09:32:18 2001

us-09-410-835-4.o11g.tbl

Page 103

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,210
FILING DATE: 23-MAR-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELETYPE: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 3973 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: m145-feature
LOCATION: 2149
OTHER INFORMATION: /note= "N=unknown nucleotide"

US-08-036-210-21
Query Match 0.31: Score 20; DB 1; Length 3973;
Best Local Similarity 100.0%; Pred. No. 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 3938 TTTATCAAAAAAAAAAAAAA 3957
|||||

RESULT 31
US-08-449-609-21
Sequence 21: Application US/08449609
Patent No. 5952112
GENERAL INFORMATION:
APPLICANT: Molter, Niels P.H.
INVENTOR: Molter, Niels P.H.
TITLE OF INVENTION: PTP-511: A NOVEL PROTEIN TYROSINE
KINASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
EIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIORITY INFORMATION:
PRIOR APPLICATION NUMBER: US 08/036,210
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELETYPE: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 3973 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: m145-feature
LOCATION: 2149
OTHER INFORMATION: /note= "N=unknown nucleotide"

Tue Mar 27 09:32:18 2001

us-09-410-835-4.o11g.tbl

Page 102

NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELETYPE: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 2692 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: m145-feature
LOCATION: 2149
OTHER INFORMATION: /note= "N=unknown nucleotide"

Query Match 0.31: Score 20; DB 2; Length 2692;
Best Local Similarity 100.0%; Pred. No. 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 2657 TTTATCAAAAAAAAAAAAAA 2676
|||||

RESULT 30
US-08-036-210-21
Sequence 21: Application US/08036210
Patent No. 5952112

GENERAL INFORMATION:
APPLICANT: Molter, Niels P.H.
INVENTOR: Molter, Niels P.H.
TITLE OF INVENTION: PTP-511: A NOVEL PROTEIN TYROSINE
KINASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
EIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

Tue Mar 27 09:32:18 2001

us-09-410-835-4.o11g.tbl

Page 104

CITY: New York
STATE: New York
COUNTRY: U.S.A.
EIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIORITY INFORMATION:
PRIOR APPLICATION NUMBER: US 08/036,210
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELETYPE: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 3973 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: m145-feature
LOCATION: 2149
OTHER INFORMATION: /note= "N=unknown nucleotide"

US-08-449-609-21
Query Match 0.31: Score 20; DB 2; Length 3973;
Best Local Similarity 100.0%; Pred. No. 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 3938 TTTATCAAAAAAAAAAAAAA 3957
|||||

RESULT 33
US-08-126-594-13/C
Sequence 13: Application US/08126594
Patent No. 5482845

GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
TITLE OF INVENTION: CONSTRUCTION OF NORMALIZED
TITLE OF INVENTION: CDNA LIBRARIES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
STREET: 10 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,594
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840/JPM/ARC
TELEPHONE: (212) 664-0520
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-126-594-13

Query Match 0.38: Score 19; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 aaaaaaaaaaaatgcct 407
DB 32 AAAAAAAAAAAATGCTT 14

Tue Mar 27 09:32:18 2001

us-09-410-835-4.0119.rml

Page 107

DB 32 AAAAAAAAAAAATGCTT 14
RESULT 34
US-08-619-5428-13/c
Sequence 13, Application US/086195428
GENERAL INFORMATION:
APPLICANT: The Trustees of Columbia University in the City
APPLICANT: of New York
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
TITLE OF INVENTION: CDNA LIBRARIES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,5428
FILING DATE: June 21, 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840-A-PCT-US
TELEPHONE: (212) 278-0400
TELEFAX: (212) 361-0525
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-619-5428-13

Query Match

0.38: Score 19; DB 2; Length 35;

Tue Mar 27 09:32:18 2001

us-09-410-835-4.0119.rml

Page 106

RESULT 33
US-08-465-811A-13/c
Sequence 13, Application US/08465811A
Patent No. 5637685
GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
TITLE OF INVENTION: CONSTRUCTION OF
TITLE OF INVENTION: NORMALIZED CDNA LIBRARIES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,811A
FILING DATE: June 6, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840/JPM/ARC
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-465-811A-13

Query Match 0.38: Score 19; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 aaaaaaaaaaaatgcct 407

Tue Mar 27 09:32:18 2001

us-09-410-835-4.0119.rml

Page 108

DB 32 AAAAAAAAAAAATGCTT 14
RESULT 35
US-07-908-245-1
Sequence 1, Application US/07908245
GENERAL INFORMATION:
APPLICANT: Harrison, David G.
APPLICANT: Alexander, R. Wayne
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF
TITLE OF INVENTION: ENDOTHELIAL NITRIC OXIDE SYNTHASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,245
FILING DATE: 1992/02
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Patel, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMU 111
TELEPHONE: 404-815-6508
TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: Bovine
Tissue Type: Aorta
Cell Type: Endothelial
US-07-908-245-1

Query Match 0.38; Score 19; DB 1; Length 4089;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 4071 TATACAGGAGGATCAAGT 1998

RESULT 16
US-09-331-581-1/c
Sequence 14, Application US/09331581
Patent No. 6130070
GENERAL INFORMATION:
APPLICANT: TONDA, Hideki
INVENTOR: TONDA, Hideki
TITLE OF INVENTION: INDUCTION PROMOTER GENE AND SECRETORY SIGNAL GENE
TITLE OF INVENTION: USABLE IN SCHISTOSOMATOSOMES POWDER, EXPRESSION VECTORS
CURRENT FILING DATE: 1999-06-30
EARLIER FILING DATE: 1998-10-31
EARLIER FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 4748
TYPE: DNA
ORGANISM: Schistosomacranocytes pombe
FEATURES: CDS
LOCATION: (2810)..(4552)
US-09-331-581-1

Query Match 0.38; Score 19; DB 3; Length 4748;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1060 atccgagcagatcaagaat 1078

Tue Mar 27 09:32:18 2001 us-09-410-835-4-0119.rml Page 111
TITLE OF INVENTION: USABLE IN SCHISTOSOMATOSOMES POWDER, EXPRESSION VECTORS
TITLE OF INVENTION: HAVING THE SAME, AND USE THEREOF
FILE REFERENCE: 0059-1142-09CT
CURRENT APPLICATION NUMBER: US/09/331,581
PRIOR APPLICATION NUMBER: 0959-06-30
EARLIER FILING DATE: 1998-10-31
EARLIER FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 7938
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence:DNA
US-09-331-581-14

Query Match 0.38; Score 19; DB 3; Length 7938;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 2016 ATCCAGCAGGATCAAGT 1998

RESULT 39
US-08-870-010A-1/c
Sequence 1, Application US/08870010A
Patent No. 6136962
GENERAL INFORMATION:
APPLICANT: SHI, Jufang
INVENTOR: Boyce-Jacino, Michael
TITLE OF INVENTION: Covalent Attachment of Unmodified
Nucleic Acids to Silanated Solid Phase Surfaces
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey & Simon
STREET: 1289 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2402
COMPUTER READABLE FORM:
OPERATING SYSTEM: IBM Compatible
SOFTWARE: PARSIO for Windows Version 2.0

DB 501 ATCCAGCAGGATCAAGT 483

RESULT 37
US-09-331-581-3/c
Sequence 14, Application US/09331581
Patent No. 6130070
GENERAL INFORMATION:
APPLICANT: TONDA, Hideki
INVENTOR: TONDA, Hideki
TITLE OF INVENTION: INDUCTION PROMOTER GENE AND SECRETORY SIGNAL GENE
TITLE OF INVENTION: USABLE IN SCHISTOSOMATOSOMES POWDER, EXPRESSION VECTORS
CURRENT FILING DATE: 1999-06-30
EARLIER FILING DATE: 1998-10-31
EARLIER FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 7286
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence:DNA
US-09-331-581-3

Query Match 0.38; Score 19; DB 3; Length 7286;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1060 atccgagcagatcaagaat 1078

RESULT 38
US-09-331-581-1/c
Sequence 14, Application US/09331581
Patent No. 6130070
GENERAL INFORMATION:
APPLICANT: TONDA, Hideki
INVENTOR: TONDA, Hideki
TITLE OF INVENTION: INDUCTION PROMOTER GENE AND SECRETORY SIGNAL GENE
TITLE OF INVENTION: HAVING THE SAME, AND USE THEREOF
CURRENT FILING DATE: 1999-06-30
EARLIER FILING DATE: 1998-10-31
EARLIER FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 7938
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence:DNA
US-09-331-581-1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,010A
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Shi, Jufang
REGISTRATION NUMBER: 39,445
TELEPHONE: 202 393-6657
TELEFAX: 202 393-6610
TELETYPE:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STANDARD: single
US-08-870-010A-1

Query Match 0.38; Score 18; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 382 attagagagagagagagag 399

RESULT 40
US-08-870-010A-1/c
Sequence 1, Application US/08870010A
Patent No. 6136962
GENERAL INFORMATION:
APPLICANT: SHI, Jufang
INVENTOR: Boyce-Jacino, Michael
TITLE OF INVENTION: Covalent Attachment of Unmodified
Nucleic Acids to Silanated Solid Phase Surfaces
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey & Simon
STREET: 1289 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2402
COMPUTER READABLE FORM:
OPERATING SYSTEM: IBM Compatible
SOFTWARE: PARSIO for Windows Version 2.0

MEDIUM TYPE: Diskette
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Pasteo for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/102.371
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Franklin S. Adams
 REGISTRATION NUMBER: 43,457
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 813-7500
 TELEFAX: (212) 813-7600
 TELETYPE:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 37 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-102-371.1

Query Match 0.38: Score 18; DB 3; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 382 attcatgataataatgct 399

DB 18 ATATACCAAAAAAAAAA 1

RESULT 41
 US-09-975-902.47
 Sequence 41: Application US/08/975.902
 Patent No. 5912148
 GENERAL INFORMATION:
 APPLICANT: Perkin-Elmer Corporation, Applied Biosystems Division
 TITLE OF INVENTION: Coupled Amplification and Ligation Method
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESS: David J. Welter, Wilson Sonsini Goodrich & Rosati
 STREET: 650 Page Mill Road
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA

Tue Mar 27 09:32:18 2001

us-09-410-835-4-olig.rml

Page 115

STATE: California
 COUNTRY: USA
 ZIP: 94304-1050
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: Microsoft Windows 98/MS-DOS 5.0
 SOFTWARE: ASCII (DOS) TEXT format
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/251.565
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/975.902
 FILING DATE: 19-SEP-96
 ATTORNEY/AGENT INFORMATION:
 NAME: David J. Welter
 REGISTRATION NUMBER: 16842-754
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 493-9300
 TELEFAX: (650) 493-9100
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 39 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-251-565.47

Query Match 0.38: Score 18; DB 3; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 389 aataataataataatgct 406

DB 5 AAAAAAAAAAATCT 22

RESULT 43
 US-08-510-032A-3/C
 Sequence 3: Application US/08510032A
 Patent No. 5721216
 GENERAL INFORMATION:
 APPLICANT: Sherman Weisman and Yairinda Prasnar
 TITLE OF INVENTION: Analysis of Gene Expression By Display of 3'-

Tue Mar 27 09:32:18 2001

us-09-410-835-4-olig.rml

Page 114

ZIP: 94304-1050
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: Microsoft Windows 3.1/MS-DOS 5.0
 SOFTWARE: Wordperfect for Windows 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/975.902
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/292.686
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: David J. Welter
 REGISTRATION NUMBER: 38,362
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 493-9300
 TELEFAX: (415) 493-9100
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 39 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-975-902.47

Query Match 0.38: Score 18; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 389 aataataataataatgct 406

DB 5 AAAAAAAAAAATCT 22

RESULT 42
 US-09-251-565.47
 Sequence 42: Application US/09251565
 Patent No. 5912148
 GENERAL INFORMATION:
 APPLICANT: Perkin-Elmer Corporation, Applied Biosystems Division
 TITLE OF INVENTION: Coupled Amplification and Ligation Method
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESS: David J. Welter, Wilson Sonsini Goodrich & Rosati
 STREET: 650 Page Mill Road
 CITY: Palo Alto

Tue Mar 27 09:32:18 2001

us-09-410-835-4-olig.rml

Page 116

TITLE OF INVENTION: end Restriction Fragments of cDNA
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESS: Yairinda Prasnar & Associates
 STREET: 25 Skytop Drive
 CITY: Stamford
 STATE: Connecticut
 ZIP: 06611
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIUM TYPE: disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Microsoft Word 4.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/510.032A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Sherman Weisman and Yairinda Prasnar
 REGISTRATION NUMBER: 36,824
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201) 261-9151
 TELEFAX: (201) 261-9151
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-510-032A-3

Query Match 0.38: Score 18; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 389 aataataataataatgct 406

DB 34 AAAAAAAAAAATCT 17

RESULT 44
 US-08-688-514-3/C
 Sequence 3: Application US/08688514
 Patent No. 6010850
 GENERAL INFORMATION:
 APPLICANT: Sherman Weisman and Yairinda Prasnar
 TITLE OF INVENTION: Analysis of Gene Expression By Display of 3'-

TITLE OF INVENTION: end Restriction Fragments of cDNA
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Tishak & Associates
 STREET: 1550 North Main Street
 CITY: Trumbull, CT 06460
 STATE: Connecticut
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/688,514
 FILING DATE:
 CLASSIFICATION: 516
 NAME: GEORGE L. YANAK
 ATTORNEY/AGENT INFORMATION:
 REFERENCE/DOCKET NUMBER: 26,824
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203)268-1951
 TELEFAX: (203)268-1951
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-688-514-3

Query Match 0.31: Score 18; DB 3; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1; 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 31 AAAAAAAAAAAAACTT 17
 QY 389 aaaaaaaaaaaaaagct 406

RESULT 45
 US-08-086-410-24
 Sequence 21: Application US/0806610
 Patent No. 5407822
 GENERAL INFORMATION:
 APPLICANT: LEPLATOIS, Pascal
 APPLICANT: LOISON, Gerard

Tue Mar 27 09:12:18 2001

us-09-410-835-4-0119.rml

Page 119

LOCATION: 109
 OTHER INFORMATION: /standard_name "a1c clat"
 FEATURE: promoter
 LOCATION: 259..270
 FEATURE: 160..163
 NAME/KEY: PATA_signal
 LOCATION: 160..163
 US-08-086-410-24

Query Match 0.31: Score 18; DB 1; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1; 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 aatgaaaaaaaaaaaaaa 402
 DB 75 AATGAAAAAAAAAAAAA 92

RESULT 46
 US-07-920-519-28
 Sequence 21: Application US/07920519
 Patent No. 5129518
 GENERAL INFORMATION:
 APPLICANT: CAPUT, DANIEL
 APPLICANT: GERMAIN, PASQUAL
 APPLICANT: RAGHAD, MOHAMED
 APPLICANT: LEGOUX, RICHARD
 APPLICANT: LOISON, GERARD
 APPLICANT: LAMBER, GUZDEN
 APPLICANT: LAMBER, GUZDEN
 APPLICANT: LEPLATOIS, PASQUAL
 APPLICANT: SALOME, MARK
 TITLE OF INVENTION: UBIATE OXIDASE ACTIVITY PROTEIN;
 TITLE OF INVENTION: RECOMBINANT CANE CODING SEQUENCE, EXPRESSION VECTOR,
 TITLE OF INVENTION: MICRO ORGANISM AND TRANSFORMED CELLS
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: POLEY & LANDNER
 STREET: 10000 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, version #1.25

Tue Mar 27 09:12:18 2001

us-09-410-835-4-0119.rml

Page 118

APPLICANT: PASSEUR, Bernard
 TITLE OF INVENTION: Artificial promoter for the expression
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: POLEY & LANDNER
 STREET: King Street Station, Suite 500, 1600 Diagonal
 CITY: ALEXANDRIA
 STATE: VIRGINIA
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/086,410
 CLASSIFICATION: 415
 NAME: PASSEUR, Bernard
 ATTORNEY/AGENT INFORMATION:
 REFERENCE/DOCKET NUMBER: 28,665
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 636-9100
 TELEFAX: (703) 683-4109
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 309 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 IMMEDIATE SOURCE:
 CLONE: AOH promoter similar to the natural AOH2
 FEATURE: promoter
 NAME/KEY: misc_binding
 LOCATION: 150
 FEATURE INFORMATION: /standard_name "a1c SpH1"
 NAME/KEY: misc_binding

Tue Mar 27 09:12:18 2001

us-09-410-835-4-0119.rml

Page 120

CURRENT APPLICATION DATA:
 FILING DATE: 05/07/920,519
 CLASSIFICATION: 415
 PRIOR APPLICATION DATA:
 FILING DATE: 05/07/659,408
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)683-4109
 TELEFAX: (703)683-4109
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 360 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: DNA (genomic)
 IMMEDIATE SOURCE:
 US-07-920-519-28
 IMMEDIATE SOURCE: a1c-mad pBR469 fragment

Query Match 0.31: Score 18; DB 1; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1; 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 aatgaaaaaaaaaaaaaa 402
 DB 79 AATGAAAAAAAAAAAAA 96

RESULT 47
 US-09-410-835-4-0119-21
 Sequence 21: Application US/0806610
 Patent No. 5407822
 GENERAL INFORMATION:
 APPLICANT: LEPLATOIS, Pascal
 APPLICANT: LOISON, GERARD
 APPLICANT: LAMBER, GUZDEN
 APPLICANT: PASSEUR, Bernard
 TITLE OF INVENTION: Artificial promoter for the expression
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: POLEY & LANDNER

1 STREET: King Street Station, Suite 500, 1800 Diagonal
2 STREET: Road PO Box 399
3 STATE: VIRGINIA
4 COUNTRY: USA
5 EIP: 22113-0259
6
7 COMPILED BY: RENDABLE FORM: 414*
8 METHOD: 1
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: Patent Release 81.0, Version 81.25
12 APPLICATION NUMBER: 09/08/086.410
13 FILING DATE:
14
15 CLASSIFICATION: 435
16 PRIOR APPLICATION DATA: US 767/66.003
17 PILING DATE: 02-OCT-1991
18 APPLICATION NUMBER: PR 89 1767
19 FILING DATE: 29-DEC-1989
20
21 NAME: AXE, Bernhard D.
22 REGISTRATION NUMBER: 28,665
23 REFERENCE/DOCKET NUMBER: 16781/318
24 TELEPHONE CATION: INNOVATION:
25 TELEPHONE: 703-681-4109
26 TELEFAX: (703) 681-4109
27
28
29 INFORMATION FOR SEQ ID NO: 21:
30
31 SEQUENCE CHARACTERISTICS: 180 base pairs
32 LENGTH: 180 base pairs
33 TYPE: nucleic acid
34 STANDARDS: double
35
36 MOLECULE TYPE: linear
37 HYPOHETICAL: NO (genomic)
38
39 IMMEDIATE SOURCE:
40
41 PLASMID: Smal-BamHI fragment
42
43 NAME/SEQ: misc-binding
44 LOCATION: 4
45
46 OTHER INFORMATION: /standard.name= "ate Klui"
47
48 NAME/SEQ: misc-binding
49 LOCATION: 154
50
51 OTHER INFORMATION: /standard.name= "ate SpH"
52
53 NAME/SEQ: misc-binding
54 LOCATION: 113
55
56 OTHER INFORMATION: /standard.name= "ate Clai"
57
58 FEATURE:

```

1 PRIOR APPLICATION DATA: US 07/659,408
2 APPLICATION NUMBER: US 07/659,408
3 PUBLICATION NO.: 1
4 ATTORNEY/AGENT INFORMATION:
5 NAME: BENT, Stephen A.
6 REGISTRATION NUMBER: 29,768
7 ADDRESS: 10000 E. 16TH AVE.
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: (703)835-9300
10 TELEFAX: (703)683-4109
11 INFORMATION FOR SEQ. ID NO.: 28:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 360 base pairs
14 TYPE: DNA (genomic)
15 TOPOLOGY: linear
16 MOLECULE TYPE: DNA (genomic)
17 PHOSPHATE: NO
18 LINKAGE: NO
19 CLONE: Plasmid pBR469 fragment
20 US-08-314566-28
21
22 Query Match 0.3% Score 18: DB 1: Length 360
23 Best Local Similarity 100.0%: Pred. No. 1.6e+02:
24 Matches 18: Conservative 0: Mismatches 0: Indels
25
26 DB 79: AAAAAAAAAAAAAAAAAAAAAA 96
27 |||

```

```

APPLICATION NUMBER: US 07/659,408
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A.
ADDRESS: 19, 188
CITY: BOSTON
STATE: MA
COUNTRY: US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)876-9100
FAX: 899142
TELEX: 969142
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
STRANDS: 2
ORIENTATION: 5' to 3'
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PRIMARY DISEASE:
IMMEDIATE SOURCE:
CLONE: pBR469 fragment
US-08-314-586-28

Query Match 0.3% Score 18: DB 1: Length 360
Query Local Similarity 100.0%: Pred. No. 1.6e+02
Matches 18: Conservative 0: Mismatches 0: Indels

DB 79 ATGTAAAAAATTTTTAAAAA 95
|||||
385 aactcaaaaataaataaataa 402
|||||

RESULT 49
US-08-686-878A-22
Sequence 22: Application US/08686878A
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Maxwell, Edward
APPLICANT: Neff, David
APPLICANT: Heiberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
TITLE OF INVENTION: 19 SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 71
SEQUENCE ADDRESSES: 71
ADDRESSER: Genetech Institute, Inc.

```


STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
FILE REFERENCE: CL-1128-A
CURRENT APPLICATION NUMBER: US/09/248,335
EARLIER FILING DATE: 08/09/98
EARLIER FILING DATE: 08/24/79
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Microsoft Word Version 7.0A
LENGTH: 861
STRANDEDNESS: double
TYPE: DNA
ORGANISM: Mammal
US-09-248-335-15

Query Match
Best Local Similarity: 100.0%; Score 18; DB 3; Length 861;
Matches: 18; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

CY 385 acgcaaaaaa 402
DB 829 aatcaaaaaa 846

RESULT 51
US-09-248-335-15
Sequence 15, Application US/09248335
Patent No. 6098504
GENERAL INFORMATION:
APPLICANT: KUGA TETSUO
APPLICANT: NAKAGAWA SATOCHI
APPLICANT: SAKAKI YOSHIOYUKI
APPLICANT: SAKAKI YOSHIOYUKI
APPLICANT: HANIDA HIDEJI
TITLE OF INVENTION: NOVEL DNA, NOVEL POLYPEPTIDE
TITLE OF INVENTION: NOVEL DNA, NOVEL POLYPEPTIDE
CORRESPONDENCE ADDRESS:
ADDRESS: FITZPATRICK, CELLA, HARPER AND SCIRNO
STREET: 217 Park Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10172-0194
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

Query Match
Best Local Similarity: 100.0%; Score 18; DB 3; Length 861;
Matches: 18; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

CY 385 acgcaaaaaa 402
DB 829 aatcaaaaaa 846

RESULT 51
US-09-248-335-15
Sequence 15, Application US/09248335
Patent No. 6098504
GENERAL INFORMATION:
APPLICANT: KUGA TETSUO
APPLICANT: NAKAGAWA SATOCHI
APPLICANT: SAKAKI YOSHIOYUKI
APPLICANT: SAKAKI YOSHIOYUKI
APPLICANT: HANIDA HIDEJI
TITLE OF INVENTION: NOVEL DNA, NOVEL POLYPEPTIDE
TITLE OF INVENTION: NOVEL DNA, NOVEL POLYPEPTIDE
CORRESPONDENCE ADDRESS:
ADDRESS: FITZPATRICK, CELLA, HARPER AND SCIRNO
STREET: 217 Park Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10172-0194
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

Query Match
Best Local Similarity: 100.0%; Score 18; DB 3; Length 882;
Matches: 18; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

CY 385 acgcaaaaaa 402
DB 829 aatcaaaaaa 843

RESULT 53
US-08-089-985C-9
Sequence 9, Application US/08089985C
Patent No. 5689599
GENERAL INFORMATION:
APPLICANT: JACOBSON ET AL.
TITLE OF INVENTION: INSECTICIDALLY EFFECTIVE SPIDER
TITLE OF INVENTION: TOXIN

APPLICANT: MICROFILM, BIRMINGHAM
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-A
CURRENT APPLICATION NUMBER: US/09/248,335
EARLIER FILING DATE: 08/09/98
EARLIER FILING DATE: 08/24/79
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Microsoft Word Version 7.0A
LENGTH: 861
STRANDEDNESS: double
TYPE: DNA
ORGANISM: Mammal
US-09-248-335-15

Query Match
Best Local Similarity: 100.0%; Score 18; DB 3; Length 861;
Matches: 18; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

CY 385 acgcaaaaaa 402
DB 829 aatcaaaaaa 846

RESULT 53
US-08-909-985C-9
Sequence 9, Application US/0809985C
Patent No. 5689599
GENERAL INFORMATION:
APPLICANT: KUGA TETSUO
APPLICANT: NAKAGAWA SATOCHI
APPLICANT: SAKAKI YOSHIOYUKI
APPLICANT: SAKAKI YOSHIOYUKI
APPLICANT: HANIDA HIDEJI
TITLE OF INVENTION: NOVEL DNA, NOVEL POLYPEPTIDE
TITLE OF INVENTION: NOVEL DNA, NOVEL POLYPEPTIDE
CORRESPONDENCE ADDRESS:
ADDRESS: FITZPATRICK, CELLA, HARPER AND SCIRNO
STREET: 217 Park Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10172-0194
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

Query Match
Best Local Similarity: 100.0%; Score 18; DB 1; Length 940;
Matches: 18; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

CY 385 acgcaaaaaa 402
DB 808 aatcaaaaaa 925

RESULT 54
US-08-457-272-1
Sequence 1, Application US/08457272
Patent No. 5689599
GENERAL INFORMATION:
APPLICANT: JACOBSON ET AL.
TITLE OF INVENTION: INSECTICIDALLY EFFECTIVE SPIDER
TITLE OF INVENTION: TOXIN

1 APPLICANT: Jackson et al.
2 TITLE OF INVENTION: INSECURITIVALLY EFFECTIVE SPIDER
3 NUMBER OF PAGES: 6
4 NUMBER OF FIGURES: 6
5 CORRESPONDENCE ADDRESS:
6 ADDRESS: Woodcock Washburn Kurtz MacIewica
7 STREET: 56535931st
8 CITY: Philadelphia
9 STATE: PA
10 COUNTRY: U.S.A.
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: 3.5 inch disk, 720 kb
13 COMPUTER: IBM PC compatible
14 SOFTWARE: 68028, PC-DOS/MS-DOS
15 SOFTWARE VERSION: 5.1
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/08/457,272
18 PRIORITY DATA:
19 PRIORITY APPLICATION DATA:
20 APPLICATION NUMBER: 08/089,998
21 FILING DATE: 07-JUL-1993
22 ATTORNEY: J. M. INDOLEKATON
23 NAME: John M. Indolekaton
24 REGISTRATION NUMBER: 26,337
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: 215-5681439
27 TELEFAX: 215-5681439
28 INFORMATION FOR SEQ ID NO: 1:
29 SEQUENCE CHARACTERISTICS:
30 TYPE: nucleic acid
31 STANDARDS: double
32 TOPOLOGY: unknown
33 15-08-457-272-1

```

Qry      385 AAAAAAAAAAAAAAAAAAAAAA 402
          1111111111111111111111111111
Db        908 AAAAAAAAAAAAAAAAAAAAAA 925

RESULT 55
ACT-US94-07595-1

```

Tue Mar 27 09:32:18 2001

us-09-410-835-4.011g.rn1

Page 131

```

RESULT 56
US-08-088-988-1
Patent No. 1,409,644
GENERAL INFORMATION:
APPLICANT: Labib, Daniel D
TITLE OF INVENTION: PHOSPHATE STAINATION-INDUCIBLE PROTEIN
FILE REFERENCE: pp196-03
CURRENT PRIORITY NUMBER: US/08/688,988
CURRENT PRIORITY NUMBER: 03-07-21
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Parsed for Windows Version 3.0
LENGTH: 1250
1. TYPE: DNA
2. SEQ ID NOS: 1-48
3. NCBI ID: AY1250
US-08-088-988-1
Anti-Dopsia Thallana

Query Match
Best Local Similarity 100 % DB 3 Length 1250
Matches 187 Conservative 0 Mismatches 0 Indels 0 Gaps 0
385 ATGTGAAAAAAAAAAAAAA 402
b 1232 ATGTGAAAAAAAAAAAAA 1249

```

RESULT 57
US-09-025-059-2
Sequence 21, Application US/09025055
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Wuegler, Neil C.
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
EIP: 94304
COMMENTS: CHINA FROM
MEDIUM TYPE: DIAXITIC
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSoft for Windows Version 2.0

Sequence 1: Application PC/70594/07595
GENERAL INFORMATION: et al
TITLE OF INVENTION: INTERMEDIATELY EFFECTIVE SPIDER
TITLE OF INVENTION: TOXIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
INVENTOR: JAMES M. COOPERATION
STREET: 1735 Main Street
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIA TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOURCE: S. 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC/70594/07595
FILING DATE: Hereafter
PRIORITY DATA:
PRIORITY APPLICATION NO.:
PRIORITY FILING DATE: 08/08/98
FILING DATE: 07 JUL 1993
ATTORNEY/AGENT INFORMATION:
NAME: Robert M. Kellough &
FIRM: Kellough, Kellough &
REGISTRATION NUMBER: 24,261 & 28,026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-299-6598
TELEFAX: 215-299-6598
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 base pairs
SEQUENCE ANALYSIS:
STRANDNESS: double
TOPOLOGY: unknown
PCR/70594-07595-1

```

Query Match      0 34: Score 18: DB 4: Length 940,
      Best Local Similarity 100.00: P-adj 1.5e-02:
      Matches 18: Conservative 0: Mismatches 0: Indels 0: Caps 0
QY 385 aatcaaaaaaaaaaaaaa 402
      |||||
Db 908 atcctaaahhhhhhhhh 925

```

Tue Mar 27 09:32:18 2001

us-09-410-835-4.011g.rn1

us-09-410-835-4.011g.rn1

Page 132

1 CURRENT APPLICATION DATA:
 2 APPLICATION NUMBER: US/09/035 059
 3 PRIORITY NUMBER: 09/035 059
 4 CLASSIFICATION:
 5 PRIOR APPLICATION DATA:
 6 APPLICATION NUMBER:
 7
 8 ATTILING DATE:
 9 ATTILING NUMBER:
 10 NAME: / Billings, Lucy J
 11 REGISTRATION NUMBER: 36,749
 12 REFERENCE/DOCNR NUMBER: PF-043 US
 13 TELECOMMUNICATION INFORMATION:
 14 TELEPHONE: 650-845-0055
 15 TELEFAX: 650-845-4166
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510

```

Query Match      0.38; Score 18; DB 3; Length 114;
Beet Local Similarity 100.00%; Prod. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY    365 aaTGTGAAAAAAAAAAAAA 402
      |||
Db    1291 AAATGAAAAAAAAAAAAAA 1298

```

05-08-210 56A-1/c
 RESULT 756
 Patient No. 5691968
 Registration US/08/700/76A
 GENERAL INFORMATION:
 APPLICANT: Sleep, Darrell
 APPLICANT: Godsey, Andrew R
 APPLICANT: Godsey, Andrew R
 TITLE OF INVENTION: "Teard Promoter"
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 SLEEP, DARRELL
 STREET: 100 HIGHLAND AVENUE, MURRAY HILL
 CITY: NEW JERSEY
 STATE: NEW JERSEY

COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Release 51.0, Version 31.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/270.076A
FILING DATE: 01-JUL-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 8923521.2
FILING DATE: 19-OCT-1989
PRIORITY APPLICATION DATA: US 07/597,687
FILING DATE: 16-OCT-1990
PRIORITY APPLICATION DATA: US 07/925,286
FILING DATE: 04-AUG-1992
NAME/KEY: R. BALD
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 24864
TELEPHONE/DOCKET NUMBER: 92834-3
TELEPHONE: 908/711-6152
TELEFAX: 908/711-6159
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
NAME/KEY: Promoter
LOCATION: 43..53
OTHER INFORMATION: /function="RNA POLIII
FEATURE:
NAME/KEY: Promoter
LOCATION: 86..96
OTHER INFORMATION: /function="RNA POLIII
FEATURE:
NAME/KEY: Promoter
LOCATION: 113..118

Tue Mar 27 09:32:18 2001

us-09-410-835-4.0119.rml

Page 135

Sequence 3 Application US/08394189B
GENERAL INFORMATION:
APPLICANT: Horvitz, Robert
APPLICANT: Yuan, Junying
TITLE OF INVENTION: EFFECTS OF HUMAN INTERLEUKIN-1
TITLE OF INVENTION: BETA CONVERSE GENE TO INHIBIT CELL DEATH
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESS: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
SOFTWARE: PC-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394.189B
FILING DATE: 24-FEB-2005
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/282,211
FILING DATE: 12-JUL-1994
APPLICATION NUMBER: 07/984,182
APPLICATION NUMBER: 07/897,788
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 113510
TELEPHONE/DOCKET NUMBER: 01997/211001
TELEPHONE: 617-428-0100
TELEFAX: 617-428-7045
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TYPE: RNA
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
NAME/KEY: Coding Sequence
LOCATION: 18...1229

Tue Mar 27 09:32:18 2001

us-09-410-835-4.0119.rml

Page 134

OTHER INFORMATION: /function="RNA POLIII
FEATURE:
NAME/KEY: Terminator
LOCATION: 1091..1103
OTHER INFORMATION: /bound.molety=
FEATURE:
NAME/KEY: Protein-bind
LOCATION: 1106..1118
OTHER INFORMATION: /bound.molety=
NAME/KEY: RAPI/GRFI/TOFI
OTHER INFORMATION: /function="pyrimidine (CT)
LOCATION: 1176..1241
OTHER INFORMATION: /block*
NAME/KEY: DATA signal
LOCATION: 1336..1335
FEATURE:
NAME/KEY: misc-signal
LOCATION: 1336..1335
OTHER INFORMATION: /function="pyrimidine (CT)
FEATURE:
NAME/KEY: misc-signal
LOCATION: 1336..1335
OTHER INFORMATION: /block*
NAME/KEY: misc-signal
LOCATION: 1336..1335
OTHER INFORMATION: /function="CAG box"
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1031..1036
OTHER INFORMATION: /function="Pati restriction site"
US-08-370-076A.1

Query Match 0.3% Score 18; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 436 TCAAAAAAAAAAATG 419
US-05-394-189B-3
RESULT 59

Tue Mar 27 09:32:18 2001

us-09-410-835-4.0119.rml

Page 136

OTHER INFORMATION: /product="human interleukin-1 beta
US-08-394-189B-3
Query Match 0.3% Score 18; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1352 AATGAAAAAAAAAAAAA 1369
RESULT 60
PCT-0593-05705-3
GENERAL INFORMATION:
APPLICANT: Human Interleukin-1
TITLE OF INVENTION: Inhibitors of cell 3 and related proteins
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Massachusetts Institute of Technology
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05705
FILING DATE: 15-JUL-1993
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1371 base pairs
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
NAME/KEY: CDS
LOCATION: 18..1232
OTHER INFORMATION: /product="human interleukin-1
OTHER INFORMATION: /convertase"

Query Match 0.3% Score 18; DB 4; Length 1373;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CORRESPONDENCE ADDRESS:
ADDRESSEE: UNUMEX CORPORATION
ATTENTION: UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION: Patent in Release #1.24
APPLICATION NUMBER: PCT/US91/03339
FILING DATE: 19910404
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSTER, HERBERT A.
REGISTRATION NUMBER: 32,585
REFERENCE/DOCKET NUMBER: 0401MO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870606
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TYPE: NUCLEIC ACID
STRANDS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
INSTRUMENT: ABI, N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
IMMEDIATE SOURCE: INTERLEUKIN 1B PROTEASE
CLONE: INTERLEUKIN 1B PROTEASE
PUBLICATION INFORMATION:
AUTHORS: BLACK, ROY
ADDRESSEE: KROEMER, SHIRLEY
PCT-US91-03339-2

Query Match 0.39: Score 18; DB 4; Length 1694;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1638 AATGAAAAAAAAAAAAA 1655

Tue Mar 27 09:32:18 2001

us-09-410-835-4.011g.rml

Page 147

Query Match 0.39: Score 18; DB 1; Length 1694;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1672 AATGAAAAAAAAAAAAA 1689

RESULT 70
US-08-607-228-9
Sequence 9, Application US/0860228
GENERAL INFORMATION:
APPLICANT: Lin, Lin-Ling
APPLICANT: Chen, Jennifer H.
APPLICANT: Chen, Jennifer H.
TITLE OF INVENTION: NOVEL TYP RECEPTOR DEATH DOMAIN LIGAND
TITLE OF INVENTION: NOVEL TYP RECEPTOR DEATH DOMAIN LIGAND
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION: Patent in Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/602,228
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G1532C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA

Tue Mar 27 09:32:18 2001

us-09-410-835-4.011g.rml

Page 146

RESULT 69
US-08-698-551-9
Sequence 9, Application US/08698551
GENERAL INFORMATION:
APPLICANT: Lin, Lin-Ling
APPLICANT: Chen, Jennifer H.
APPLICANT: Chen, Jennifer H.
TITLE OF INVENTION: NOVEL TYP RECEPTOR DEATH DOMAIN LIGAND
TITLE OF INVENTION: NOVEL TYP RECEPTOR DEATH DOMAIN LIGAND
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION: Patent in Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/698,551
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G1532D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
INSTRUMENT: ABI, N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
IMMEDIATE SOURCE: INTERLEUKIN 1B PROTEASE
CLONE: INTERLEUKIN 1B PROTEASE
PUBLICATION INFORMATION:
AUTHORS: BLACK, ROY
ADDRESSEE: KROEMER, SHIRLEY
PCT-US91-03339-2

Tue Mar 27 09:32:18 2001

us-09-410-835-4.011g.rml

Page 146

Query Match 0.39: Score 18; DB 2; Length 1694;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1672 AATGAAAAAAAAAAAAA 1689

RESULT 71
US-08-494-440B-9
Sequence 9, Application US/0849440B
GENERAL INFORMATION:
APPLICANT: Lin, Lin-Ling
APPLICANT: Chen, Jennifer H.
APPLICANT: Chen, Jennifer H.
TITLE OF INVENTION: NOVEL TYP RECEPTOR DEATH DOMAIN LIGAND
TITLE OF INVENTION: NOVEL TYP RECEPTOR DEATH DOMAIN LIGAND
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION: Patent in Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/494,440B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G1532A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 9:

TITLE OF INVENTION: PROTEINS AND INHIBITORS OF LIGAND BINDING
NUMBER OF SEQUENCES: 14
COMPLETION DATE: 1999-01-01
ADDRESS: Cambridge Institute, Inc.
STREET: 87 Cambridge Park Drive
CITY: Cambridge
STATE: Massachusetts
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
SOFTWARE: 8086/8088 DOS
CURRENT APPLICATION DATA: Patent Released 41.0, Version 41.25
APPLICATION NUMBER: PCT/US95/12174
CLASSIFICATION:
FILING DATE: 1995-07-14
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,721
TELEPHONE: (617) 488-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1694 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLWEIGHT: 1000000
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
START: 1
END: 1694
PCT-US95-12174-9

Query Match 0.38: Score 18: DB 4: Length 1694:
Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 1672 ATGTGAAAGAAAAA 402
DB 1672 ATGTGAAAGAAAAA 1699

RESULT 76
US 6411646-1
Sequence 1, Application US/07841646

PILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 22-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 22-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 212,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDWARD R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CIP-0001C6
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1801
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLWEIGHT: 1000000
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
START: 1
END: 1801
PCT-US95-12174-9

Query Match 0.38: Score 18: DB 1: Length 1801:
Matches 18: Conservative 100.0%: Pct No. 1.4e+02:
Best Local Similarity 100.0%: Pct No. 1.4e+02:

PATENT NO. 5266683
GENERAL INFORMATION:
APPLICANT: OBERMAN, HERMAN
APPLICANT: OBERMAN, ENGIN
APPLICANT: RUBEN, DAVID C.
APPLICANT: RUBEN, DAVID C.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 13
COMPLETION DATE: 1999-01-01
ADDRESS: RUBEN, DAVID C. & RUBEN, DAVID C.
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
SOFTWARE: 8086/8088 DOS
CURRENT APPLICATION DATA: Patent Released 41.0, Version 41.25
APPLICATION NUMBER: US/07/841,646
CLASSIFICATION:
FILING DATE: 1995-07-14
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,721
TELEPHONE: (617) 488-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1694 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLWEIGHT: 1000000
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
START: 1
END: 1694
PCT-US95-12174-9

Query Match 0.38: Score 18: DB 1: Length 1801:
Matches 18: Conservative 100.0%: Pct No. 1.4e+02:
Best Local Similarity 100.0%: Pct No. 1.4e+02:

PILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 22-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 22-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 212,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDWARD R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CIP-0001C6
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1801
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLWEIGHT: 1000000
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
START: 1
END: 1801
PCT-US95-12174-9

Query Match 0.38: Score 18: DB 1: Length 1801:
Matches 18: Conservative 100.0%: Pct No. 1.4e+02:
Best Local Similarity 100.0%: Pct No. 1.4e+02:

ORGANISM: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
FEATURE: CDS
LOCATION: 49..1341
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= 'OSTEOGENIC PROTEIN'
OTHER INFORMATION: /product= 'OPT'
OTHER INFORMATION: /standard_name= 'OPT'
US-07-901-703-1

Query Match 0.31; Score 18; DB 1; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1801 AATGCAAAAAAAAAAAAAA 1818

RESULT 78

US-08-147-023-1

Sequence 1, Application US/08147023
Patent No. 5468845
INVENTOR: OPPENHEIM, HERMAN
APPLICANT: OPPENHEIM, HERMAN
APPLICANT: OKRAYNA, ERIC
APPLICANT: KUBERANATHAN, THANGAVEL
APPLICANT: RIEBER, DAVID C.
APPLICANT: RIEBER, DAVID C.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESS: 555A, HODWITZ & THIBEAULT
STREET 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
CONTACT: 010-514-230-1100
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: STRINGS, Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08147-023
FILING DATE: 21-FEB-1992
CLASSIFICATION: 3510
PRIORITY INFORMATION:
PRIOR APPLICATION DATA:

Tue Mar 27 09:12:18 2001

us-09-410-835-4.o11g.rml

Page 159

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: HOMO SAPIENS
ORIGINAL SOURCE:
TISSUE TYPE: HIPPOCAMPUS
FEATURES:
NAME/KEY: CDS
LOCATION: 49..1341
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= 'OSTEOGENIC PROTEIN'
OTHER INFORMATION: /product= 'OPT'
OTHER INFORMATION: /standard_name= 'OPT'
US-08-147-023-1

Query Match 0.31; Score 18; DB 1; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1801 AATGCAAAAAAAAAAAAAA 1818

RESULT 79

US-08-206-864-1

Sequence 1, Application US/08206864
Patent No. 5468845
INVENTOR: JONES, WILLIAM K
APPLICANT: JONES, WILLIAM K
APPLICANT: OKRAYNA, ERIC
APPLICANT: KUBERANATHAN, THANGAVEL
APPLICANT: RIEBER, DAVID C.
APPLICANT: RIEBER, DAVID C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESS: 555A, HODWITZ & THIBEAULT
STREET 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
CONTACT: 010-514-230-1100
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: STRINGS, Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08206-864
CLASSIFICATION: 510
PRIORITY INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027-070
FILING DATE: 04-MAR-1993
APPLICATION NUMBER: US 07/841,646
FILING DATE: 21-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDWARD R.
REGISTRATION NUMBER: 27,828
REFERENCE/DOCKET NUMBER: CRP-096
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
FAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: HOMO SAPIENS
ORIGINAL SOURCE:
TISSUE TYPE: HIPPOCAMPUS
FEATURE: CDS
LOCATION: 49..1341
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= 'OSTEOGENIC PROTEIN'
OTHER INFORMATION: /product= 'OPT'
OTHER INFORMATION: /standard_name= 'OPT'
US-08-206-864-1

Query Match 0.31; Score 18; DB 1; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue Mar 27 09:12:18 2001

us-09-410-835-4.o11g.rml

Page 158

APPLICATION NUMBER: US 810,560
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA: US 179,460
FILING DATE: 15-AUG-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDWARD R.
REGISTRATION NUMBER: 27,828
REFERENCE/DOCKET NUMBER: CRP-096
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
FAX: 617/248-7100

Tue Mar 27 09:12:18 2001

us-09-410-835-4.o11g.rml

Page 160

07 385 AATGAAAAAAAAAAAAA 402
DB 1801 AATGAAAAAAAAAAAAA 1818

RESULT 80
US-08-278-729A-16
Sequence 16, Application US/08278729A
Patent No. 5650276

GENERAL INFORMATION:
APPLICANT: OPERMAN, HERMAN
APPLICANT: OZAYANAK, ENGIN
APPLICANT: KUBERASAPATH, THANCAVEL
APPLICANT: ROGER, DAVID C.
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PATENT IN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,729A
CLASSIFICATION: 435-9001
CILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER Esq., EDWARD R.
REGISTRATION NUMBER: 27,829
TELEPHONE: (508) 435-9001
TELEFAX: (508) 435-9951
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: cDNA
FEATURE:

Tue Mar 27 09:12:18 2001 us-09-410-835-4.olly.rml

Page 163

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
NAME/REV: CDS
LOCATION: 49..1341
OTHER INFORMATION: /function="OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product="NOP1-PP"
OTHER INFORMATION: /note="NOP1 cDNA"
US-08-480-528A-3

Query Match 0.34; Score 18; DB 1; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 385 AATGAAAAAAAAAAAAA 402
DB 1801 AATGAAAAAAAAAAAAA 1818

RESULT 82
US-08-479-666-3
Sequence 3, Application US/08479666
Patent No. 5653337

GENERAL INFORMATION:
APPLICANT: OPERMAN, HERMAN
APPLICANT: OZAYANAK, ENGIN
APPLICANT: KUBERASAPATH, THANCAVEL
APPLICANT: ROGER, DAVID C.
APPLICANT: COHEN, CHARLES M.
APPLICANT: PANG, ROY H.T.
TITLE OF INVENTION: OSTEOGENIC PROTEIN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PATENT IN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:

Tue Mar 27 09:12:18 2001

us-09-410-835-4.olly.rml

Page 162

NAME/REV: CDS
LOCATION: 49..1341
OTHER INFORMATION: /product="NOP1-PP"
US-08-278-729A-16

Query Match 0.34; Score 18; DB 1; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 385 AATGAAAAAAAAAAAAA 402
DB 1801 AATGAAAAAAAAAAAAA 1818

RESULT 81
US-08-480-528A-3
Sequence 3, Application US/08480528A
Patent No. 5652118

GENERAL INFORMATION:
APPLICANT: OPERMAN, HERMAN
APPLICANT: OZAYANAK, ENGIN
APPLICANT: KUBERASAPATH, THANCAVEL
APPLICANT: ROGER, DAVID C.
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: OSTEOGENIC PROTEIN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PATENT IN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,528A
CLASSIFICATION: 435-9001
CILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: FENTON Esq., GILLIAN M.
REGISTRATION NUMBER: 36,508
TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100

Tue Mar 27 09:12:18 2001 us-09-410-835-4.olly.rml

Page 164

APPLICATION NUMBER: US/08/479,666
PATENT NO. 5653337
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FENTON Esq., GILLIAN M.
REGISTRATION NUMBER: 36,508
TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
NAME/REV: CDS
LOCATION: 49..1341
OTHER INFORMATION: /function="OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product="NOP1-PP"
OTHER INFORMATION: /note="NOP1 cDNA"
US-08-479-666-3

Query Match 0.34; Score 18; DB 1; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 385 AATGAAAAAAAAAAAAA 402
DB 1801 AATGAAAAAAAAAAAAA 1818

RESULT 83

US-08-155-343A-16
Sequence 16, Application US/08155343A
Patent No. 5653337

GENERAL INFORMATION:
APPLICANT: KUBERASAPATH, THANCAVEL
APPLICANT: ROGER, DAVID C.
APPLICANT: OPERMAN, HERMAN
APPLICANT: OZAYANAK, ENGIN
APPLICANT: PANG, ROY H.T.
TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET 45 SOUTH STREET

CITY: HOPKINTON
STATE: MA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 15-NOV-1993
PRIORITY APPLICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FERTON ESQ. GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-067FW
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDS
LOCATION: 49..1341
OTHER INFORMATION: /product= "HOP-1"

US-08-406-672-16

Query Match 0.34; Score 18; DB 1; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 385 aatgaataaataaataa 402
DB 1801 AATGAAATAAATAA 1818

RESULT 84
US-08-406-672-16
Sequence 1: Application US/08406672
Patent No. 56744844
GENERAL INFORMATION:
APPLICANT: KOBERSANAPATH, THANGAVEL
APPLICANT: COHEN, CHARLES M
APPLICANT: OPPENHAIN, HERMANN

Tue Mar 27 09:32:18 2001 us-09-410-835-4.011g.rml Page 167

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 385 aatgaataaataaataa 402
DB 1801 AATGAAATAAATAA 1818

RESULT 85
US-08-406-672-16
Sequence 1: Application US/08643563A
Patent No. 5707810
GENERAL INFORMATION:
APPLICANT: SMART, JOHN
APPLICANT: OPPENHAIN, HERMANN
APPLICANT: OKRAYMAN, ENGIN
APPLICANT: KOBERSANAPATH, THANGAVEL
APPLICANT: RUDGER, DAVID C.
APPLICANT: PANG, ROY H. L. M
APPLICANT: COHEN, CHARLES M
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
FILING DATE: 06-MAY-1996
PRIORITY APPLICATION:
ATTORNEY/AGENT INFORMATION:
NAME: TOWNE ESQ. MICHAEL J.
REGISTRATION NUMBER: 38,349
REFERENCE/DOCKET NUMBER: CRP-058CZ
TELEPHONE: (508) 435-6901
TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

APPLICANT: OKRAYMAN, ENGIN
APPLICANT: RUDGER, DAVID C.
APPLICANT: PANG, ROY H. L. M
TITLE OF INVENTION: TREATMENT TO PREVENT LOSS OF AND/OR
INCREASE BONE MASS IN METABOLIC BONE DISEASES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
FILING DATE: 06-MAY-1996
PRIORITY APPLICATION:
ATTORNEY/AGENT INFORMATION:
NAME: TOWNE ESQ. MICHAEL J.
REGISTRATION NUMBER: 38,349
REFERENCE/DOCKET NUMBER: CRP-066CN
TELEPHONE: (508) 435-6901
TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDS
LOCATION: 49..1341
OTHER INFORMATION: /product= "HOP-1"

US-08-406-672-16

Query Match 0.34; Score 18; DB 1; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 385 aatgaataaataaataa 402
DB 1801 AATGAAATAAATAA 1818

Tue Mar 27 09:32:18 2001 us-09-410-835-4.011g.rml Page 168

FEATURES:
NAME/KEY: CDS
LOCATION: 49..1341
OTHER INFORMATION: /product= "HOP-1"

US-08-643-563A-16

Query Match 0.34; Score 18; DB 1; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 385 aatgaataaataaataa 402
DB 1801 AATGAAATAAATAA 1818

RESULT 86
US-08-447-570-1
Sequence 1: Application US/08447570
Patent No. 5714599
GENERAL INFORMATION:
APPLICANT: OPPENHAIN, HERMANN
APPLICANT: OKRAYMAN, ENGIN
APPLICANT: KOBERSANAPATH, THANGAVEL
APPLICANT: RUDGER, DAVID C.
APPLICANT: PANG, ROY H. L. M
APPLICANT: COHEN, CHARLES M
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: 45 SOUTH STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
FILING DATE: 21-FEB-1992
PRIORITY APPLICATION:
ATTORNEY/AGENT INFORMATION:
NAME: TOWNE ESQ. MICHAEL J.
REGISTRATION NUMBER: 38,349
REFERENCE/DOCKET NUMBER: CRP-058CZ
TELEPHONE: (508) 435-6901
TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

ANTI-SENSE: NO
ORIGINAL SOURCE: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
NAME/KEY: CDS
LOCATION: 49.1341
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function="osteogenic protein"
OTHER INFORMATION: /evidence="EXPERIMENTAL"
OTHER INFORMATION: /standard_name="OP1"
US-08-449-700-1

Query Match 0.31; Score 18; DB 2; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1801 AAAAAAAAAAAAAAAAAA 1818

RESULT 95
US-08-449-699A-1
Sequence 1, Application US/08/449699A
Patent No. 5968411
GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OKAYAMA, ENGIN
APPLICANT: KUBERMANPATH, THANGAVEL
APPLICANT: RUBER, DAVID C.
APPLICANT: NISHITOH, HIDETI
TITLE OF INVENTION: ANTIBODIES TO OSTEOGENIC PROTEINS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: SHWITT & THIBEAULT
STREET 125 HIGH STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
FILING DATE: 24-MAY-1995
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release 11.0, Version 11.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,699A
FILING DATE: 24-MAY-1995

Tue Mar 27 09:12:18 2001

us-09-410-835-4.0119.rml

Page 183

TITLE OF INVENTION: NOVEL SIGNALING RECEPTOR FOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: SHWITT & THIBEAULT
STREET 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release 11.0, Version 11.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,268B
FILING DATE: 13
ATTORNEY/AGENT INFORMATION:
NAME: METERS, THOMAS C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: CRP-117
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDS
LOCATION: 49.1341
OTHER INFORMATION: /product="OP1"
OTHER INFORMATION: /standard_name="OP1"
US-08-696-268B-3

Query Match 0.31; Score 18; DB 2; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1801 AAAAAAAAAAAAAAAAAA 1818

Tue Mar 27 09:12:18 2001

us-09-410-835-4.0119.rml

Page 182

CLASSIFICATION: 424
PROTEIN INFORMATION:
APPLICATION NUMBER: US 08/447,023
FILING DATE: 01-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,929
REFERENCE/DOCKET NUMBER: STP-001CP6CH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
FEATURES:
NAME/KEY: CDS 1341
LOCATION: 49.1341
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function="osteogenic protein"
OTHER INFORMATION: /evidence="EXPERIMENTAL"
OTHER INFORMATION: /standard_name="OP1"
US-08-449-699A-1

Query Match 0.31; Score 18; DB 2; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1801 AAAAAAAAAAAAAAAAAA 1818

RESULT 96
US-08-696-268B-3
Sequence 3, Application US/08696268B
Patent No. 5968752
GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: KUBERMANPATH, THANGAVEL
APPLICANT: RUBER, DAVID C.
APPLICANT: NISHITOH, HIDETI
APPLICANT: SANPATH, KUBER T.
TITLE OF INVENTION: NOVEL SIGNALING RECEPTOR FOR
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: SHWITT & THIBEAULT
STREET 125 HIGH STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
FILING DATE: 24-MAY-1995
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release 11.0, Version 11.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,397A
FILING DATE: 13
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,929
REFERENCE/DOCKET NUMBER: STP-074PM2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7000
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURES:
NAME/KEY: CDS 1341
LOCATION: 49.1341
OTHER INFORMATION: /product="OP1"
OTHER INFORMATION: /standard_name="OP1"
US-08-461-397A-16

Tue Mar 27 09:12:18 2001

us-09-410-835-4.0119.rml

Page 184

RESULT 97
US-08-461-397A-16
Sequence 16, Application US/08461397A
Patent No. 5972884
GENERAL INFORMATION:
APPLICANT: COHEN, CHARLES M.
APPLICANT: KUBERMANPATH, THANGAVEL
APPLICANT: RUBER, DAVID C.
APPLICANT: OPPERMANN, HERMANN
APPLICANT: PANG, ROY H. L.
APPLICANT: NISHITOH, HIDETI
APPLICANT: SMART, JOHN E.
TITLE OF INVENTION: NOVEL TREATMENT FOR LIMITING
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: SHWITT & THIBEAULT
STREET 125 HIGH STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
FILING DATE: 13
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,929
REFERENCE/DOCKET NUMBER: STP-074PM2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7000
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURES:
NAME/KEY: CDS 1341
LOCATION: 49.1341
OTHER INFORMATION: /product="OP1"
OTHER INFORMATION: /standard_name="OP1"
US-08-461-397A-16

QY 385 aatgagaaagaaagaaagaa 402
DB 1801 aatgagaaagaaagaaagaa 1818

RESULT 104
US-09-410-835-4-0119-1
Sequence 3: Application US/08459129
Patent No. 6110482
GENERAL INFORMATION:
APPLICANT: RUGER, ROGER K.
INVENTOR: RUGER, ROGER K.
APPLICANT: RUGER, ROGER K.
TITLE OF INVENTION: MANUFACTURE OF AUTOGENOUS REPLACEMENT
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESS: 1527A HURWITZ & THIBEAULT
STREET: 51 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08459129
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
PRIORITY DATE:
ATTORNEY/AGENT INFORMATION:
NAME: REILEY, ROBIN D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-101
TELEPHONE: 617/248-7100
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDNA
LOCATION: 49..1341
OTHER INFORMATION: /function="OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product="OP1"
OTHER INFORMATION: /evidence="EXPERIMENTAL"
OTHER INFORMATION: /standard_name="OP1"
OTHER INFORMATION: /standard_name="OP1"

Tue Mar 27 09:32:18 2001

us-09-410-835-4-0119.rml

Page 195

CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/901,200
PRIORITY DATE: 09/01/97
ATTORNEY/AGENT INFORMATION:
NAME: METERS, THOMAS C.
REGISTRATION NUMBER: 16,989
REFERENCE/DOCKET NUMBER: CRP-076DV2
TELEPHONE: (508) 435-5901
TELEFAX: (508) 435-5931
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDNA
LOCATION: 49..1341
OTHER INFORMATION: /function="OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product="OP1"
OTHER INFORMATION: /evidence="EXPERIMENTAL"
OTHER INFORMATION: /standard_name="OP1"

US-09-410-835-4-0119-1
Query Match 0.31, Score 18, DB 3, Length 1822;
Best Local Similarity 100.0%; Pred. No. 14e+02;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 aatgagaaagaaagaaagaa 402
DB 1801 aatgagaaagaaagaaagaa 1818

RESULT 106
PCT-US90-07654-3
Sequence 3: Application PC/TUS9007654
GENERAL INFORMATION:
APPLICANT: RUGER, ROGER K.
INVENTOR: RUGER, ROGER K.
APPLICANT: RUGER, ROGER K.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESSES:
ADDRESS: 1527A HURWITZ & THIBEAULT
STREET: 51 STATE STREET
CITY: BOSTON
STATE: MA

Tue Mar 27 09:32:18 2001

us-09-410-835-4-0119.rml

Page 194

ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
FEATURE:
NAME/KEY: CDG 1341
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function="OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product="OP1"
OTHER INFORMATION: /evidence="EXPERIMENTAL"
OTHER INFORMATION: /standard_name="OP1"
OTHER INFORMATION: /standard_name="OP1"

US-08-459-129-1
Query Match 0.31, Score 18, DB 3, Length 1822;
Best Local Similarity 100.0%; Pred. No. 14e+02;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 aatgagaaagaaagaaagaa 402
DB 1801 aatgagaaagaaagaaagaa 1818

RESULT 105
US-09-410-835-4-0119-1
Sequence 3: Application US/09219391
Patent No. 6133583
GENERAL INFORMATION:
APPLICANT: RUGER, ROGER K.
INVENTOR: RUGER, ROGER K.
APPLICANT: RUGER, ROGER K.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESS: 1527A HURWITZ & THIBEAULT
STREET: 51 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09219391
FILING DATE:

Tue Mar 27 09:32:18 2001

us-09-410-835-4-0119.rml

Page 196

COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/07654
FILING DATE: 19901228
CLASSIFICATION: 156
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/901,200
PRIORITY DATE: 09/01/97
ATTORNEY/AGENT INFORMATION:
NAME: METERS, THOMAS C.
REGISTRATION NUMBER: 16,989
REFERENCE/DOCKET NUMBER: CRP-001P5
TELEPHONE: (508) 435-5901
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDNA
LOCATION: 49..1341
OTHER INFORMATION: /function="OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product="OP1"
OTHER INFORMATION: /evidence="EXPERIMENTAL"
OTHER INFORMATION: /standard_name="OP1"

PCT-US90-07654-3
Query Match 0.31, Score 18, DB 4, Length 1822;
Best Local Similarity 100.0%; Pred. No. 14e+02;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 aatgagaaagaaagaaagaa 402
DB 1801 aatgagaaagaaagaaagaa 1818

RESULT 107

PCT-US91-07635-1
Sequence 1: Application PC/TUS9107635
GENERAL INFORMATION:
APPLICANT: OBERMANN, HERMAN
INVENTOR: OBERMANN, HERMAN
APPLICANT: KUBERASAMATH, THANCAVEL
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: 33 STATE STREET
ADDRESS: TESTA, HERWITZ & THIBEAULT
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release 1.0, Version 1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07635
CLASSIFICATION: 1911018
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-052PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7100
FILING DATE: 11-MAR-1991
LENGTH: 1822 base pairs
SEQUENCE CHARACTERISTICS:
TYPE: NUCLEIC ACID
STRANDS: single
MOLECULE TYPE: CDNA
HYPOTHEMETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
FEATURE:
NAME/KEY: CDS 1341
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: //function="OSTEOGENIC PROTEIN"
OTHER INFORMATION: //product="OPT"
OTHER INFORMATION: //evidence="EXPERIMENTAL"

TELEPHONE: 617/248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: NUCLEIC ACID
STRANDS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHEMETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
FEATURE/KEY: CDS
LOCATION: 49..1341
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: //function="OSTEOGENIC PROTEIN"
OTHER INFORMATION: //product="OPT"
OTHER INFORMATION: //evidence="EXPERIMENTAL"
OTHER INFORMATION: //standard_name="OPT"
PCT-US92-01968-16

Query Match 0.35, Score 18, DB 4, Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 385 atcagcaaaaaaaaaaaaaa 402
DB 1801 atcagcaaaaaaaaaaaaaa 1818
RESULT 109
PCT-US93-05446-1
Sequence 1: Application PC/TUS9305446
GENERAL INFORMATION:
TITLE OF INVENTION: PROSTHETIC DEVICES HAVING ENHANCED
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS: 33 STATE STREET
ADDRESS: TESTA, HERWITZ & THIBEAULT
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OTHER INFORMATION: //standard_name="OPT"
PCT-US91-07635-1
Query Match 0.35, Score 18, DB 4, Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 385 atcagcaaaaaaaaaaaaaa 402
DB 1801 atcagcaaaaaaaaaaaaaa 1818
RESULT 108
PCT-US92-01968-16
Sequence 1: Application PC/TUS9201968
GENERAL INFORMATION:
APPLICANT: COHEN, CHARLES H
INVENTOR: COHEN, CHARLES H
APPLICANT: KUBERASAMATH, THANCAVEL
TITLE OF INVENTION: PROTEIN-INDUCED MORPHOGENESIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: 33 STATE STREET
ADDRESS: TESTA, HERWITZ & THIBEAULT
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release 1.0, Version 1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/01968
CLASSIFICATION: 1927011
FILING DATE: 11-MAR-1991
PRIORITY INFORMATION:
APPLICATION NUMBER: US 667,274
FILING DATE: 11-MAR-1991
APPLICATION NUMBER: US 752,764
FILING DATE: 10-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-052PC
TELECOMMUNICATION INFORMATION:

OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05446
FILING DATE: 19930608
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STX-057
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: 11/248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: NUCLEIC ACID
STRANDS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHEMETICAL: NO
ORIGINAL SOURCE: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
FEATURE/KEY: CDS
LOCATION: 49..1341
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: //function="OSTEOGENIC PROTEIN"
OTHER INFORMATION: //product="OPT"
OTHER INFORMATION: //evidence="EXPERIMENTAL"
OTHER INFORMATION: //standard_name="OPT"
PCT-US93-05446-1

Query Match 0.35, Score 18, DB 4, Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 385 atcagcaaaaaaaaaaaaaa 402
DB 1801 atcagcaaaaaaaaaaaaaa 1818
RESULT 110
PCT-US93-07189-1
Sequence 1: Application PC/TUS9307189
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MORPHOGENIC PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS: 33 STATE STREET
ADDRESS: TESTA, HERWITZ & THIBEAULT
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR/CREATIVE BIOMOLECULES,
ADDRESS: 1801
STREET: 35 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US93/07189
PCT DATE: 19930729
CLASSIFICATION:
PRIORITY INFORMATION:
PRIORITY APPLICATION NUMBER:
PRIORITY APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATTORNEY NAME: ROBIN D. KELLEY
REGISTRATION NUMBER: 314,637
REFERENCE/DOCKET NUMBER: 314,637
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
MOL WT: 1872 base pairs
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
FEATURE: TYPE: HIPPOCAMPUS
NAME/KEY: CDS
LOCATION: 49..1141
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function="OSTROGENIC PROTEIN"
OTHER INFORMATION: /product="TOP1"
OTHER INFORMATION: /evidence="EXPERIMENTAL"
OTHER INFORMATION: /standard_name="TOP1"
PCT-US93-07189-1

Query Match 0.38; Score 18; DB 4; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue Mar 27 09:32:18 2001

us-09-410-835-4.019.mtl

Page 203

OTHER INFORMATION: /product="TOP1"
OTHER INFORMATION: /evidence="EXPERIMENTAL"
OTHER INFORMATION: /standard_name="TOP1"
PCT-US93-07190-16
Query Match 0.38; Score 18; DB 4; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1801 AATGAAAAAAAAAAAAA 1818

RESULT 112
PCT-US93-07231-16
Sequence 16, Application PC/TUS9307231
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MORPHOGEN-INDUCED NERVE REGENERATION AND
METHOD OF INVENTION: REPAIR
ADDRESSEE: CREATIVE BIOMOLECULES, INC.
STREET: 35 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US93/07231
PCT DATE: 19930729
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY NAME: ROBIN D. KELLEY
REGISTRATION NUMBER: 314,637
REFERENCE/DOCKET NUMBER: 314,637
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
FAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

OTHER INFORMATION: /product="TOP1"
OTHER INFORMATION: /evidence="EXPERIMENTAL"
OTHER INFORMATION: /standard_name="TOP1"
PCT-US93-07190-16
Query Match 0.38; Score 18; DB 4; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1801 AATGAAAAAAAAAAAAA 1818

Tue Mar 27 09:32:18 2001

us-09-410-835-4.019.mtl

Page 202

Query 385 AATGAAAAAAAAAAAAA 402
DB 1801 AATGAAAAAAAAAAAAA 1818
RESULT 111
PCT-US93-07190-16
Sequence 16, Application PC/TUS9307190
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MORPHOGEN-ENRICHED DIFRAN COMPOSITION
METHOD OF INVENTION: REPAIR
ADDRESSEE: CREATIVE BIOMOLECULES, INC.
STREET: 35 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US93/07190
PCT DATE: 19930729
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY NAME: ROBIN D. KELLEY
REGISTRATION NUMBER: 314,637
REFERENCE/DOCKET NUMBER: 314,637
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
FAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOL WT: 1872 base pairs
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
FEATURE: TYPE: HIPPOCAMPUS
NAME/KEY: CDS
LOCATION: 49..1141
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function="OSTROGENIC PROTEIN"
OTHER INFORMATION: /product="TOP1"
OTHER INFORMATION: /evidence="EXPERIMENTAL"
OTHER INFORMATION: /standard_name="TOP1"
PCT-US93-07231-16

Query Match 0.38; Score 18; DB 4; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1801 AATGAAAAAAAAAAAAA 1818

RESULT 113
PCT-US93-08742-16
Sequence 16, Application PC/TUS9308742
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MORPHOGEN-INDUCED PERIODONTAL TISSUE REGENERATION
METHOD OF INVENTION: REPAIR
ADDRESSEE: CREATIVE BIOMOLECULES, INC.
STREET: 35 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US93/08742
PCT DATE: 19930729
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY NAME: ROBIN D. KELLEY
REGISTRATION NUMBER: 314,637
REFERENCE/DOCKET NUMBER: 314,637
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
FAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

OTHER INFORMATION: /product="TOP1"
OTHER INFORMATION: /evidence="EXPERIMENTAL"
OTHER INFORMATION: /standard_name="TOP1"
PCT-US93-07231-16
Query Match 0.38; Score 18; DB 4; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1801 AATGAAAAAAAAAAAAA 1818

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY ESQ. ROBIN D.
REGISTRATION NUMBER: 34,637
TELEPHONE: 617/248-7100
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
FEATURE:
NAME/KEY: CDS
LOCATION: 49..1341
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function="OSTROGENIC PROTEIN"
OTHER INFORMATION: /product="OP1"
OTHER INFORMATION: /evidence="EXPERIMENTAL"
OTHER INFORMATION: /standard_name="OP1"
PCT-US93-08742-16

Query Match
Best Local Similarity: 100.0%; Pred. No. 1,4e+02;
Matches: 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 aatgaataaataaataa 402
DB 1801 aatgaataaataaataa 1818

RESULT 114
PCT-US93-08808-16
Sequence 16, Application PC/TUS9308808
GENERAL INFORMATION:
TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: CREATIVE BIOMOLECULES, INC.
STREET: 45 SOUTH STREET
CITY: HOKKINGTON
STATE: MA
COUNTRY: USA

Tue Mar 27 09:32:18 2001

us-09-410-835-4-011g.rml

Page 207

DB 1801 aatgaataaataaataa 1818

RESULT 115
PCT-US93-08885-16
Sequence 16, Application PC/TUS9308885
GENERAL INFORMATION:
TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: CREATIVE BIOMOLECULES, INC.
STREET: 45 SOUTH STREET
CITY: HOKKINGTON
STATE: MA
COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release 11.0, Version 11.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08885
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY ESQ. ROBIN D.
REGISTRATION NUMBER: 34,637
TELEPHONE: 617/248-7100
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
FEATURE:

Tue Mar 27 09:32:18 2001

us-09-410-835-4-011g.rml

Page 206

CITY: HOKKINGTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release 11.0, Version 11.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08808
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY ESQ. ROBIN D.
REGISTRATION NUMBER: 34,637
TELEPHONE: 617/248-7100
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
FEATURE:
NAME/KEY: CDS
LOCATION: 49..1341
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function="OSTROGENIC PROTEIN"
OTHER INFORMATION: /product="OP1"
OTHER INFORMATION: /evidence="EXPERIMENTAL"
OTHER INFORMATION: /standard_name="OP1"
PCT-US93-08808-16

Query Match
Best Local Similarity: 100.0%; Pred. No. 1,4e+02;
Matches: 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 aatgaataaataaataa 402
DB 1801 aatgaataaataaataa 1818

RESULT 116
PCT-US93-10520-3
Sequence 3, Application PC/TUS9310520
GENERAL INFORMATION:
TITLE OF INVENTION: OP3-INDUCED MORPHOGENESIS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: CREATIVE BIOMOLECULES, INC.
STREET: 45 SOUTH STREET
CITY: HOKKINGTON
STATE: MA
COUNTRY: USA

Tue Mar 27 09:32:18 2001

us-09-410-835-4-011g.rml

Page 208

NAME/KEY: CDS
LOCATION: 49..1341
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function="OSTROGENIC PROTEIN"
OTHER INFORMATION: /product="OP1"
OTHER INFORMATION: /evidence="EXPERIMENTAL"
OTHER INFORMATION: /standard_name="OP1"
PCT-US93-08885-16

Query Match
Best Local Similarity: 100.0%; Pred. No. 1,4e+02;
Matches: 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 aatgaataaataaataa 402
DB 1801 aatgaataaataaataa 1818

RESULT 116
PCT-US93-10520-3
Sequence 3, Application PC/TUS9310520
GENERAL INFORMATION:
TITLE OF INVENTION: OP3-INDUCED MORPHOGENESIS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: CREATIVE BIOMOLECULES, INC.
STREET: 45 SOUTH STREET
CITY: HOKKINGTON
STATE: MA
COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release 11.0, Version 11.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10520
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,274
FILING DATE: 10-AUG-1991
APPLICATION DATA: US 07/752,764
FILING DATE: 30-AUG-1991
APPLICATION DATA: US 07/753,059
FILING DATE: 30-AUG-1991

Prior Application Data:
Application Number: US 07/752,857
Filing Date: 30 Nov-1991
Priority Date: 30 Nov-1991
Application Number: US 07/923,780
Filing Date: 31-Jul-1992
Priority Date: 31-Jul-1992
Prior Application Data: US 07/923,813
Filing Date: 31-Jul-1992
Priority Date: 31-Jul-1992
Attorney/Agent Information:
Name: PITCHER, ESQ., EDWARD R.
Registration Number: 27,829
Address: 1000 N. GARDEN ST., SUITE 100
TELEPHONE: (508) 435-9001
TELECOMMUNICATION INFORMATION:
Information for SEQ ID NO: 3:
Sequence Characteristics:
Type: nucleic acid
Strandedness: single
Topology: linear
Molecule Type: cDNA
Hypothetical: NO
Original Source:
Organism: HOMO SAPIENS
Feature:
Name/Key: CDS
Location: 49..1341
Identification Method: experimental
Other Information: /product="HOP1-PP"
Other Information: /note="HOP1 cDNA"
PCT-0593-10530-3

Query Match 0.38; Score 18; DB 4; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 385 aatgaaataaataaataa 402
DB 1801 AATGAAAAAAAAAAAAA 1818

RESULT 117
PCT-0593-05467-9
Sequence 9, Application PC/TUS9505467
General Information:
Name/Key: CDS
Location: 49..1341
Identification Method: experimental
Other Information: /product="HOP1-PP"
Other Information: /note="HOP1 cDNA"
PCT-0593-05467-9

Tue Mar 27 09:12:18 2001 us-09-410-835-4.o11g.rml
DB 1801 AATGAAAAAAAAAAAAA 1818
Page 211

RESULT 118
PCT-0593-06724-1
Sequence 1, Application PC/TUS9506724
General Information:
Name/Key: CDS
Location: 49..1341
Identification Method: experimental
Other Information: /product="HOP1-PP"
Other Information: /note="HOP1 cDNA"
PCT-0593-06724-1
Title of Invention: MANUFACTURE OF AUTOCOMPLEMENTARY
Title of Invention: BODY PARTS
Number of Sequences: 3
Correspondence Address:
Address: 31 STATE STREET
City: BOSTON
State: MA
Country: USA
ZIP: 02109
Computer Readable Form:
Medium Type: floppy disk
Computer: IBM PC compatible
Software: PC-GENE/MS-DOS
Current Application Data:
Application Number: PCT/US95/06724
Filing Date: 1998-09-09
Priority Date: 1998-09-09
Prior Application Data:
Application Number:
Filing Date:
Attorney/Agent Information:
Name: PITCHER, ESQ., EDWARD R.
Registration Number: 27,829
Address: 1000 N. GARDEN ST., SUITE 100
TELEPHONE: (508) 435-9001
TELECOMMUNICATION INFORMATION:
Information for SEQ ID NO: 1:
Sequence Characteristics:
Type: nucleic acid
Strandedness: single
Topology: linear
Molecule Type: cDNA
Hypothetical: NO
Original Source:
Organism: HOMO SAPIENS
Tissue Type: HIPPOCAMPUS
Feature:

Application:
Title of Invention: NONGENOMIC PROTEIN-SPECIFIC CELL
SURFACE RECEPTORS AND USES THEREFOR
Number of Sequences: 15
Correspondence Address:
Address: 31 STATE STREET
City: BOSTON
State: MA
Country: USA
ZIP: 02109
Computer Readable Form:
Medium Type: floppy disk
Computer: IBM PC compatible
Software: PC-GENE/MS-DOS
Current Application Data:
Application Number: PCT/US95/05467
Filing Date: 1998-09-09
Priority Date: 1998-09-09
Prior Application Data:
Application Number:
Filing Date:
Attorney/Agent Information:
Name: PITCHER, ESQ., EDWARD R.
Registration Number: 27,829
Address: 1000 N. GARDEN ST., SUITE 100
TELEPHONE: (508) 435-9001
TELECOMMUNICATION INFORMATION:
Information for SEQ ID NO: 9:
Sequence Characteristics:
Type: nucleic acid
Strandedness: single
Topology: linear
Molecule Type: cDNA
Hypothetical: NO
Original Source:
Organism: HOMO SAPIENS
Feature:
Name/Key: CDS
Location: 49..1341
Identification Method: experimental
Other Information: /product="HOP1-PP"
Other Information: /note="HOP1 cDNA"
PCT-0593-05467-9

Query Match 0.38; Score 18; DB 4; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 385 aatgaaataaataaataa 402
DB 1801 AATGAAAAAAAAAAAAA 1818

RESULT 119
PCT-0593-06724-1
Sequence 6, Application US/09150133B
General Information:
Name/Key: CDS
Location: 49..1341
Identification Method: experimental
Other Information: /product="HOP1-PP"
Other Information: /note="HOP1 cDNA"
PCT-0593-06724-1
Title of Invention: MANUFACTURE OF AUTOCOMPLEMENTARY
Title of Invention: BODY PARTS
Number of Sequences: 3
Correspondence Address:
Address: 31 STATE STREET
City: BOSTON
State: MA
Country: USA
ZIP: 02109
Computer Readable Form:
Medium Type: floppy disk
Computer: IBM PC compatible
Software: PC-GENE/MS-DOS
Current Application Data:
Application Number: PCT/US95/06724
Filing Date: 1998-09-09
Priority Date: 1998-09-09
Prior Application Data:
Application Number:
Filing Date:
Attorney/Agent Information:
Name: PITCHER, ESQ., EDWARD R.
Registration Number: 27,829
Address: 1000 N. GARDEN ST., SUITE 100
TELEPHONE: (508) 435-9001
TELECOMMUNICATION INFORMATION:
Information for SEQ ID NO: 6:
Sequence Characteristics:
Type: nucleic acid
Strandedness: single
Topology: linear
Molecule Type: cDNA
Hypothetical: NO
Original Source:
Organism: HOMO SAPIENS
Tissue Type: HIPPOCAMPUS
Feature:

Query Match 0.38; Score 18; DB 4; Length 1822;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 385 aatgaaataaataaataa 402
DB 1801 AATGAAAAAAAAAAAAA 1818

RESULT 120
US-09-150-141-6
Sequence 6, Application US/09150141B
General Information:
Name/Key: CDS
Location: 49..1341
Identification Method: experimental
Other Information: /product="HOP1-PP"
Other Information: /note="HOP1 cDNA"
PCT-0593-06724-1
Title of Invention: MANUFACTURE OF AUTOCOMPLEMENTARY
Title of Invention: BODY PARTS
Number of Sequences: 3
Correspondence Address:
Address: 31 STATE STREET
City: BOSTON
State: MA
Country: USA
ZIP: 02109
Computer Readable Form:
Medium Type: floppy disk
Computer: IBM PC compatible
Software: PC-GENE/MS-DOS
Current Application Data:
Application Number: PCT/US95/06724
Filing Date: 1998-09-09
Priority Date: 1998-09-09
Prior Application Data:
Application Number:
Filing Date:
Attorney/Agent Information:
Name: PITCHER, ESQ., EDWARD R.
Registration Number: 27,829
Address: 1000 N. GARDEN ST., SUITE 100
TELEPHONE: (508) 435-9001
TELECOMMUNICATION INFORMATION:
Information for SEQ ID NO: 6:
Sequence Characteristics:
Type: nucleic acid
Strandedness: single
Topology: linear
Molecule Type: cDNA
Hypothetical: NO
Original Source:
Organism: HOMO SAPIENS
Tissue Type: HIPPOCAMPUS
Feature:

Query Match 0.38; Score 18; DB 3; Length 1855;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 3261 accatttcgcgcgaagt 3778
DB 673 accatttcgcgcgaagt 6590

GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMAN
APPLICANT: OKAYNAK, ENGIN
APPLICANT: KUBERSHAPATH, THANGAVEL
APPLICANT: RIEBER, DAVID C.
APPLICANT: PANG, ROY H.L. C.
TITLE OF INVENTION: OSTEOGENIC DEVICES
ADDRESS: 1000 ROUTE 1
ADDRESS: 1000 ROUTE 1
ADDRESS: 1000 ROUTE 1
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.35
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/0147,023
FILING DATE: 18-OCT-1990
CLASSIFICATION: 510-1592
PRIORITY INFORMATION:
PRIORITY APPLICATION NUMBER: US 810,560
PRIORITY APPLICATION DATE: 28-DEC-1991
PRIORITY APPLICATION NUMBER: US 827,052
PRIORITY APPLICATION DATE: 28-JAN-1992
PRIORITY APPLICATION NUMBER: US 660,162
PRIORITY APPLICATION DATE: 23-FEB-1991
PRIORITY APPLICATION NUMBER: US 621,988
PRIORITY APPLICATION DATE: 04-DEC-1990
PRIORITY APPLICATION NUMBER: US 621,849
PRIORITY APPLICATION DATE: 04-DEC-1990
PRIORITY APPLICATION NUMBER: US 616,374
PRIORITY APPLICATION DATE: 12-NOV-1990
PRIORITY APPLICATION NUMBER: US 600,024
PRIORITY APPLICATION DATE: 18-OCT-1990
PRIORITY APPLICATION NUMBER: US 599,543
PRIORITY APPLICATION DATE: 18-OCT-1990
PRIORITY APPLICATION NUMBER: US 579,865
PRIORITY APPLICATION DATE: 07-SEP-1990

Tue Mar 27 09:32:18 2001

us-09-410-835-4-0119.mtl

Page 219

US-08-278-729A-18
Sequence 18, Application US/08278729A
Patent No. 5550376
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMAN
APPLICANT: OKAYNAK, ENGIN
APPLICANT: KUBERSHAPATH, THANGAVEL
APPLICANT: RIEBER, DAVID C.
APPLICANT: PANG, ROY H.L. C.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
ADDRESS: 1000 ROUTE 1
ADDRESS: 1000 ROUTE 1
ADDRESS: 1000 ROUTE 1
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/278,729A
FILING DATE: 18-OCT-1990
CLASSIFICATION: 510-1592
PRIORITY INFORMATION:
PRIORITY APPLICATION NUMBER: US 810,560
PRIORITY APPLICATION DATE: 28-DEC-1991
PRIORITY APPLICATION NUMBER: US 827,052
PRIORITY APPLICATION DATE: 28-JAN-1992
PRIORITY APPLICATION NUMBER: US 660,162
PRIORITY APPLICATION DATE: 23-FEB-1991
PRIORITY APPLICATION NUMBER: US 621,988
PRIORITY APPLICATION DATE: 04-DEC-1990
PRIORITY APPLICATION NUMBER: US 621,849
PRIORITY APPLICATION DATE: 04-DEC-1990
PRIORITY APPLICATION NUMBER: US 616,374
PRIORITY APPLICATION DATE: 12-NOV-1990
PRIORITY APPLICATION NUMBER: US 600,024
PRIORITY APPLICATION DATE: 18-OCT-1990
PRIORITY APPLICATION NUMBER: US 599,543
PRIORITY APPLICATION DATE: 18-OCT-1990
PRIORITY APPLICATION NUMBER: US 579,865
PRIORITY APPLICATION DATE: 07-SEP-1990

Query Match

0.31; Score 18; DB 1; Length 1873;

Tue Mar 27 09:32:18 2001

us-09-410-835-4-0119.mtl

Page 216

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 18-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 15-AUG-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 08-APR-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDWARD R.
REFERENCE/DOCKET NUMBER: 27,429
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
FAX: 617/248-7100
SEQUENCE CHARACTERISTICS:
LENGTH: 1873 base pairs
TYPE: nucleic acid
TOPOLGIC TYPE: single
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 104-1393
OTHER INFORMATION: /function="OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product="MOP1"
OTHER INFORMATION: /note="MOP1 CDNA"
US-08-147-023-24
Query Match
0.31; Score 18; DB 1; Length 1873;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 385 aatgaataaataaataa 402
DB 1835 aatgaataaataaataa 1852
RESULT 124
US-08-480-528A-5
Sequence 5, Application US/08480528A
Patent No. 5551118
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMAN
APPLICANT: OKAYNAK, ENGIN
APPLICANT: KUBERSHAPATH, THANGAVEL
APPLICANT: RIEBER, DAVID C.
APPLICANT: PANG, ROY H.L. C.
TITLE OF INVENTION: OPT-INDUCED MORPHOGENESIS
ADDRESS: 1000 ROUTE 1
ADDRESS: 1000 ROUTE 1
ADDRESS: 1000 ROUTE 1
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/480,528A
FILING DATE: 18-OCT-1990
CLASSIFICATION: 510-1592
PRIORITY INFORMATION:
PRIORITY APPLICATION NUMBER: US 810,560
PRIORITY APPLICATION DATE: 28-DEC-1991
PRIORITY APPLICATION NUMBER: US 827,052
PRIORITY APPLICATION DATE: 28-JAN-1992
PRIORITY APPLICATION NUMBER: US 660,162
PRIORITY APPLICATION DATE: 23-FEB-1991
PRIORITY APPLICATION NUMBER: US 621,988
PRIORITY APPLICATION DATE: 04-DEC-1990
PRIORITY APPLICATION NUMBER: US 621,849
PRIORITY APPLICATION DATE: 04-DEC-1990
PRIORITY APPLICATION NUMBER: US 616,374
PRIORITY APPLICATION DATE: 12-NOV-1990
PRIORITY APPLICATION NUMBER: US 600,024
PRIORITY APPLICATION DATE: 18-OCT-1990
PRIORITY APPLICATION NUMBER: US 599,543
PRIORITY APPLICATION DATE: 18-OCT-1990
PRIORITY APPLICATION NUMBER: US 579,865
PRIORITY APPLICATION DATE: 07-SEP-1990

Tue Mar 27 09:32:18 2001

us-09-410-835-4-0119.mtl

Page 220

Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 385 aatgaataaataaataa 402
DB 1835 aatgaataaataaataa 1852
RESULT 125
US-08-480-528A-5
Sequence 5, Application US/08480528A
Patent No. 5551118
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMAN
APPLICANT: OKAYNAK, ENGIN
APPLICANT: KUBERSHAPATH, THANGAVEL
APPLICANT: RIEBER, DAVID C.
APPLICANT: PANG, ROY H.L. C.
TITLE OF INVENTION: OPT-INDUCED MORPHOGENESIS
ADDRESS: 1000 ROUTE 1
ADDRESS: 1000 ROUTE 1
ADDRESS: 1000 ROUTE 1
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/480,528A
FILING DATE: 18-OCT-1990
CLASSIFICATION: 510-1592
PRIORITY INFORMATION:
PRIORITY APPLICATION NUMBER: US 810,560
PRIORITY APPLICATION DATE: 28-DEC-1991
PRIORITY APPLICATION NUMBER: US 827,052
PRIORITY APPLICATION DATE: 28-JAN-1992
PRIORITY APPLICATION NUMBER: US 660,162
PRIORITY APPLICATION DATE: 23-FEB-1991
PRIORITY APPLICATION NUMBER: US 621,988
PRIORITY APPLICATION DATE: 04-DEC-1990
PRIORITY APPLICATION NUMBER: US 621,849
PRIORITY APPLICATION DATE: 04-DEC-1990
PRIORITY APPLICATION NUMBER: US 616,374
PRIORITY APPLICATION DATE: 12-NOV-1990
PRIORITY APPLICATION NUMBER: US 600,024
PRIORITY APPLICATION DATE: 18-OCT-1990
PRIORITY APPLICATION NUMBER: US 599,543
PRIORITY APPLICATION DATE: 18-OCT-1990
PRIORITY APPLICATION NUMBER: US 579,865
PRIORITY APPLICATION DATE: 07-SEP-1990

Query Match

0.31; Score 18; DB 1; Length 1873;

Tue Mar 27 09:32:18 2001

US-09-410-835-4, 0119, PD

```

1      PILING DATE: 04-DEC-1990
2      PRIOR APPLICATION DATA: US 616,374
3      PILING DATE: 21-NOV-1990
4      PRIOR APPLICATION NUMBER: US 600,024
5      PRIOR APPLICATION DATA:
6      PILING DATE: 18-OCT-1990
7      PRIOR APPLICATION NUMBER: US 599,543
8      PRIOR APPLICATION DATA:
9      PILING DATE: 07-SEP-1990
10     PILING DATE: 07-SEP-1990
11     PRIOR APPLICATION NUMBER: US 569,920
12     PRIOR APPLICATION DATA:
13     PILING DATE: 22-FEB-1990
14     PRIOR APPLICATION NUMBER: US 481,913
15     PRIOR APPLICATION DATA:
16     PILING DATE: 11-OCT-1989
17     PRIOR APPLICATION NUMBER: US 422,613
18     PRIOR APPLICATION DATA:
19     PILING DATE: 12-FEB-1989
20     PRIOR APPLICATION NUMBER: US 315,342
21     PRIOR APPLICATION DATA:
22     PILING DATE: 15-AUG-1988
23     PRIOR APPLICATION NUMBER: US 232,630
24     PRIOR APPLICATION DATA:
25     PILING DATE: 08-APR-1988
26     PRIOR APPLICATION NUMBER: US 179,460
27     PRIOR APPLICATION DATA:
28     NAME: PITCHER, EDMUND R.
29     ADDRESS: 17230
30     REFERENCE/DOCUMENT NUMBER: 1,7230
31     TELECOMMUNICATION INFORMATION:
32     TELEPHONE: 617/248-7000
33     TELEFAX: 617/248-1100
34     SEQUENCE CHARACTERISTICS: 24.
35     LENGTH: 1873 base pairs
36     TYPE: nucleic acid
37     STRANDED: single
38     TOPOLOGY: linear
39     FEATURE:
40     NAME: CDS
41     LOCATION: 100..1393
42     OTHER INFORMATION: /function="OSTROSCOPIC PROTEIN"
43     OTHER INFORMATION: /product="WOP1"
44     OTHER INFORMATION: /note="WOP1 CDNA"

```

Query Match Similarity 0.3% Score 18: DB 1: Length 1873:
 Matched 1/0 ConverterActive 0/ Mismatched 0/ Indels 0/ Caps 0

385 aaaaaaaaaaaaaaaaaa 402
 Db 1835 aaaaaaaaaaaaaaaaaa 1852

RESULT 130
 Sequence 124 1835-1370-24
 Patent No. 5714589
 GENERAL INFORMATION:
 APPLICANT: OPPERMAN, HERMAN
 APPLICANT: KUBERSAWATHI, THINAWEL
 APPLICANT: RUGER, DAVID C.
 APPLICANT: KING, ROY H. L.
 APPLICANT: HANCOCK, GEODESIC DEVICES
 NUMBER OF INVENTORS: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSER: TESTA, MORITZ & TRIBAULT
 STREET: 513 STATE STREET
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: U. S. A.
 ZIP: 02108
 COMMENTS: 1. ANALOG FORM;
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION IN RELEASE #1.0, Version #1.35
 APPLICATION NUMBER: US/06/441,570
 FILING DATE: 21-FEB-1993
 CLASSIFICATION: 356
 PENDING PRIORITY DATA:
 APPLICATION NUMBER: US 810,560
 FILING DATE: 20-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 827,052
 FILING DATE: 21-FEB-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 660,162
 FILING DATE: 22-FEB-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 621,988
 FILING DATE: 04-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 621,849

Tue Mar 27 09:32:18 2001

us-09-410-835-4.011g.rn1

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDS
LOCATION: 104, 1393
OTHER INFORMATION: /product= "MOP1 (CDNA)"
US-08-643-763A-18

Query Match
Best Local Similarity 100.0% Score 18; DB 1; Length 1873;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 aatgaataaataaataa 402
DB 1835 AATGAATAAATAAATAA 1852

RESULT 112
US-08-623-18
Sequence 18; Application US/0846233
GENERAL INFORMATION:
PATENT NUMBER: 5741641
INVENTOR: COHEN, CHARLES M.
APPLICANT: COHEN, CHARLES M.
APPLICANT: KOBERSAMPAH, THANGAVEL
APPLICANT: OPPEN, DAVID C.
APPLICANT: OPPEN, DAVID C.
APPLICANT: OPPEN, DAVID C.
APPLICANT: OPPEN, DAVID C.
TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
DISEASES
TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
DISEASES
NUMBER OF SEQUENCES: 11
ADDRESS: 45 SOUTH STREET
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION IN RELEASE #1.0, Version #1.30
APPLICATION NUMBER: US/0846233
FILING DATE: 28-MAY-1993

Thu Mar 27 09:12:18 2001

us-09-410-835-4.01lg.rml

Page 231

US-08-451-953A-18
OTHER INFORMATION: /product= "MOP1 (CDNA)"
US-08-451-953A-18
LOCATION: 104, 1393
NAME/KEY: CDS
FEATURES:
NAME/KEY: CDS
LOCATION: 104, 1393
OTHER INFORMATION: /product= "MOP1 (CDNA)"
US-08-451-953A-18
Query Match
Best Local Similarity 100.0% Score 18; DB 1; Length 1873;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 aatgaataaataaataa 402
DB 1835 AATGAATAAATAAATAA 1852

RESULT 114
US-08-459-346-3
Sequence 3; Application US/08459346
GENERAL INFORMATION:
PATENT NUMBER: 5741641
INVENTOR: COHEN, CHARLES M.
APPLICANT: COHEN, CHARLES M.
APPLICANT: KOBERSAMPAH, THANGAVEL
APPLICANT: OPPEN, DAVID C.
APPLICANT: OPPEN, DAVID C.
APPLICANT: OPPEN, DAVID C.
TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
DISEASES
TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
DISEASES
NUMBER OF SEQUENCES: 11
ADDRESS: 45 SOUTH STREET
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION IN RELEASE #1.0, Version #1.30
APPLICATION NUMBER: US/08459346
FILING DATE: 28-MAY-1993

Thu Mar 27 09:12:18 2001

us-09-410-835-4.01lg.rml

Page 230

CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/445,882
FILING DATE: 12-SEP-1993
INVENTOR: COHEN, CHARLES M.
APPLICANT: COHEN, CHARLES M.
APPLICANT: KOBERSAMPAH, THANGAVEL
APPLICANT: OPPEN, DAVID C.
APPLICANT: OPPEN, DAVID C.
APPLICANT: OPPEN, DAVID C.
TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
DISEASES
TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
DISEASES
NUMBER OF SEQUENCES: 11
ADDRESS: 45 SOUTH STREET
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION IN RELEASE #1.0, Version #1.30
APPLICATION NUMBER: US/08459346
FILING DATE: 28-MAY-1993

Thu Mar 27 09:12:18 2001

us-09-410-835-4.01lg.rml

Page 232

US-08-451-953A-18
OTHER INFORMATION: /product= "MOP1 (CDNA)"
US-08-451-953A-18
LOCATION: 104, 1393
NAME/KEY: CDS
FEATURES:
NAME/KEY: CDS
LOCATION: 104, 1393
OTHER INFORMATION: /product= "MOP1 (CDNA)"
US-08-451-953A-18
Query Match
Best Local Similarity 100.0% Score 18; DB 1; Length 1873;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 aatgaataaataaataa 402
DB 1835 AATGAATAAATAAATAA 1852

RESULT 113
US-08-451-953A-18
Sequence 18; Application US/08451953A
GENERAL INFORMATION:
PATENT NUMBER: 5741641
INVENTOR: COHEN, CHARLES M.
APPLICANT: COHEN, CHARLES M.
APPLICANT: KOBERSAMPAH, THANGAVEL
APPLICANT: OPPEN, DAVID C.
APPLICANT: OPPEN, DAVID C.
APPLICANT: OPPEN, DAVID C.
TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
DISEASES
TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
DISEASES
NUMBER OF SEQUENCES: 11
ADDRESS: 45 SOUTH STREET
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION IN RELEASE #1.0, Version #1.30
APPLICATION NUMBER: US/08451953A
FILING DATE: 28-MAY-1993

FILED DATE: 15-AUG-1988
PRIORITY APPLICATION NUMBER: US 119,460
FILING DATE: 08-APR-1988
NAME/AGENT INFORMATION:
REGISTRATION NUMBER: 27,829
TELEPHONE/DOCKET NUMBER: 617/248-7000
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1873 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 104..1193
OTHER INFORMATION: /function="OSTROGENIC PROTEIN"
OTHER INFORMATION: /product="MOP1 CDNA"
US-08-449-700-24

Query Match
Best Local Similarity: 0.31; Score 18; DB 2; Length 1873;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1835 ATCTGAAAAAAAAAAAAA 1852

RESULT 138
US-08-449-699A-24
Sequence 2: 595941
Patent No. 595941
GENERAL INFORMATION:
APPLICANT: OPERMAN, HERMAN
APPLICANT: OKAYMAN, ENGIN
APPLICANT: KUBERSAMPATH, THANGAVEL
APPLICANT: RUGER, DAVID C.
APPLICANT: PANG, ROY H. L.
TITLE OF INVENTION: ANTIOXIDANTS TO OSTROGENIC PROTEINS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSER: TESTA UNIVERSITY & THIRDAULT
STREET: 125 HIGH STREET

PATENT NO. 597284
GENERAL INFORMATION:
APPLICANT: COHEN, CHARLES M.
APPLICANT: CHARETTE, MARC P.
APPLICANT: KUBERSAMPATH, THANGAVEL
APPLICANT: RUGER, DAVID C.
APPLICANT: PANG, ROY H. L.
APPLICANT: OKAYMAN, ENGIN
APPLICANT: SMART, JOHN E.
TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITING
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSER: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.30
FILING DATE: 05-JUN-1995
ATTORNEY/LOCATION: 514
NAME: PITCHER ESQ., EDWARD R.
REGISTRATION NUMBER: 27,829
TELEPHONE/DOCKET NUMBER: 617/248-7000
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1873 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 104..1193
OTHER INFORMATION: /product="MOP1 CDNA"
US-08-461-397A-18

Query Match
0.31; Score 18; DB 2; Length 1873;

US-08-461-397A-18

Tue Mar 27 09:32:18 2001

us-09-410-835-4.01lg.rml

Page 239

Tue Mar 27 09:32:18 2001

us-09-410-835-4.01lg.rml

Page 238

CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.25
FILING DATE: 05-JUN-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/147,023
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDWARD R.
REGISTRATION NUMBER: 27,829
TELEPHONE/DOCKET NUMBER: 617/248-7000
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1873 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 104..1193
OTHER INFORMATION: /function="OSTROGENIC PROTEIN"
OTHER INFORMATION: /product="MOP1 CDNA"
US-08-449-699A-24

Query Match

Best Local Similarity: 0.31; Score 18; DB 2; Length 1873;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1835 ATCTGAAAAAAAAAAAAA 1852

RESULT 139
US-08-461-397A-18
Sequence 18: Application US/08461397A

Tue Mar 27 09:32:18 2001

us-09-410-835-4.01lg.rml

Page 240

Query Match

Best Local Similarity: 0.31; Score 18; DB 2; Length 1873;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1835 ATCTGAAAAAAAAAAAAA 1852

RESULT 140
US-08-461-397A-18
Sequence 18: Application US/08461397A

PATENT NO. 597284
GENERAL INFORMATION:
APPLICANT: COHEN, CHARLES M.
APPLICANT: CHARETTE, MARC P.
APPLICANT: KUBERSAMPATH, THANGAVEL
APPLICANT: RUGER, DAVID C.
APPLICANT: PANG, ROY H. L.
APPLICANT: OKAYMAN, ENGIN
APPLICANT: SMART, JOHN E.
TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITING
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSER: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.30
FILING DATE: 05-JUN-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/147,023
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ., EDWARD R.
REGISTRATION NUMBER: 27,829
TELEPHONE/DOCKET NUMBER: 617/248-7000
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1873 base pairs

NAME: CDS
LOCATION: 104.1393
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product= "MOP1 (CDNA)"
US-08-410-835-4.0119.rml

Query Match 0.38; Score 18; DB 3; Length 1873;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1835 AATCAAAAAAAAAA 402
1835 AATCAAAAAAAAAA 1852

RESULT 144
US-08-460-515A-18
Sequence 1: Application US/08460515A
Patent No. 6100373
GENERAL INFORMATION:
APPLICANT: KUBERSAMPATH, THANGAVEL
APPLICANT: PANG, ROY H.L.
APPLICANT: HERMANN, HERMANN
APPLICANT: COHEN, CHARLES M.
APPLICANT: SHART, JOHN E. M.
TITLE OF INVENTION: MORPHOGEN TREATMENT OF ORGAN TRANSPLANTS
NUMBER OF INVENTORS: 3
CORRESPONDENCE ADDRESS:
STREET: 45 SOUTH STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02148
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 05/08/1995
CLASSIFICATION: 415.1595
ATTORNEY/AGENT INFORMATION:
NAME: GILLIN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-068FVC

Tue Mar 27 09:32:18 2001

us-09-410-835-4.0119.rml

Page 247

CURRENT APPLICATION DATA:
FILING DATE: 05/09/219.391
CLASSIFICATION:
PRIORITY APPLICATION DATA:
PRIORITY NUMBER: US 08/901,200
ATTORNEY/AGENT INFORMATION:
NAME: HERGENROTHER, THOMAS
REGISTRATION NUMBER: 36,989
TELEPHONE: (908) 415-6390
TELEFAX: (908) 415-6390
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1873
TYPE: Nucleic Acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDS
LOCATION: 104.1393
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product= "MOP1 (CDNA)"
OTHER INFORMATION: /note= "MOP1 (CDNA)"
US-09-219-391-5

Query Match 0.38; Score 18; DB 3; Length 1873;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1835 AATCAAAAAAAAAA 402
1835 AATCAAAAAAAAAA 1852

RESULT 145
PCT-US90-07654-1
Sequence 1: Application PC/US9007654
Patent No. 6100373
GENERAL INFORMATION:
APPLICANT: OKAYAMA, ENGIN
APPLICANT: KUBERSAMPATH, THANGAVEL
APPLICANT: HERMANN, HERMANN
APPLICANT: COHEN, CHARLES M.
APPLICANT: SHART, JOHN E. M.
TITLE OF INVENTION: MORPHOGEN TREATMENT OF ORGAN TRANSPLANTS
NUMBER OF INVENTORS: 3
CORRESPONDENCE ADDRESS:
STREET: 45 SOUTH STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02148
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 05/08/1995
CLASSIFICATION: 415.1595
ATTORNEY/AGENT INFORMATION:
NAME: GILLIN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-068FVC

Tue Mar 27 09:32:18 2001

us-09-410-835-4.0119.rml

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
FAX: (617) 248-7100
SEQUENCE INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1873
TYPE: Nucleic Acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDS
LOCATION: 104.1393
OTHER INFORMATION: /product= "MOP1 (CDNA)"
OTHER INFORMATION: /note= "MOP1 (CDNA)"
US-08-460-515A-18

Query Match 0.38; Score 18; DB 3; Length 1873;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1835 AATCAAAAAAAAAA 402
1835 AATCAAAAAAAAAA 1852

RESULT 145
US-08-215391-5
Sequence 5: Application US/09215391
Patent No. 6151563
GENERAL INFORMATION:
APPLICANT: OKAYAMA, ENGIN
APPLICANT: KUBERSAMPATH, THANGAVEL
APPLICANT: HERMANN, HERMANN
APPLICANT: COHEN, CHARLES M.
APPLICANT: SHART, JOHN E. M.
TITLE OF INVENTION: MORPHOGEN TREATMENT OF ORGAN TRANSPLANTS
NUMBER OF INVENTORS: 3
CORRESPONDENCE ADDRESS:
STREET: 45 SOUTH STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02148
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

us-09-410-835-4.0119.rml

Tue Mar 27 09:32:18 2001

us-09-410-835-4.0119.rml

Page 248

STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
OPERATING SYSTEM: IBM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19901228
CLASSIFICATION: 415.1595
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, ROBERT
REGISTRATION NUMBER: 37,129
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1873
TYPE: Nucleic Acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDS
LOCATION: 104.1393
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product= "MOP1 (CDNA)"
OTHER INFORMATION: /note= "MOP1 (CDNA)"
PCT-US90-07654-1

Query Match 0.38; Score 18; DB 3; Length 1873;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1835 AATCAAAAAAAAAA 402
1835 AATCAAAAAAAAAA 1852

RESULT 146
PCT-US90-07654-1
Sequence 1: Application PC/US9007654
Patent No. 6100373
GENERAL INFORMATION:
APPLICANT: OKAYAMA, ENGIN
APPLICANT: KUBERSAMPATH, THANGAVEL
APPLICANT: HERMANN, HERMANN
APPLICANT: COHEN, CHARLES M.
APPLICANT: SHART, JOHN E. M.
TITLE OF INVENTION: MORPHOGEN TREATMENT OF ORGAN TRANSPLANTS
NUMBER OF INVENTORS: 3
CORRESPONDENCE ADDRESS:
STREET: 45 SOUTH STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02148
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 05/08/1995
CLASSIFICATION: 415.1595
ATTORNEY/AGENT INFORMATION:
NAME: GILLIN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-068FVC

PC/0592-01968-18
Sequence 18, Application PC/059201968
GENERAL INFORMATION:
APPLICANT: COHEN, CHARLES M
APPLICANT: BERNHARDT, THANGAVEL
APPLICANT: PIERCE, ROBERT
APPLICANT: OPPENHAIN, HERMAN
APPLICANT: BRUCKER, DAVID C
TITLE OF INVENTION: PROTEIN-INDUCED MORPHOGENESIS
IN VITRO
CORRESPONDENCE ADDRESS:
ADDRESSER: TESTI, RUMWITZ & THIBOUT
STREET: EXCHANGE PLACE 53 STATE STREET
CITY: BOSTON
STATE: MASS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM: 4145
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
APPLICATION DATA:
FILING DATE: 19920311
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 567,274
FILING DATE: 11-MAR-1992
PRIOR APPLICATION DATA: US 752,764
APPLICATION NUMBER: US 752,764
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDWARD R
REGISTRATION NUMBER: 27,899
REFERENCE/DOCKET NUMBER: CRP-053PC
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
TYPE: NUCLEIC ACID, PLAS
STANDARDS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: HUMAN
ANTI-SENSE: NO
ORIGINAL SOURCE:
TISSUE TYPE: EMBRIO

Tue Mar 27 09:32:18 2001

us-09-410-835-4.0119.rtf

```

QY      385 acgcaaaaaaaaaa 402
          |||||
Db      1035 ATTCAATAAAAAAA 1052
          |||||
Query Match      100.00%
Seq. Identity     100.00%
Pos. Identity     100.00%
Score 101.4602
Length 1873
Mismatches 0
Conservative 0
Indels 0
Gaps 0

```

RESULT 149
PCT-US93-07189-3
; Sequence 3, Application PC/TUS9307189
; GENERAL INFORMATION:

1 TITLE OF INVENTION: NOVEL MOSPHOPHONIC PROTEIN COMPOSITION
2
3 TITLE OF INVENTION: NOVEL MOSPHOPHONIC PROTEIN COMPOSITION
4 OF MATTER
5 CORRESPONDENCE ADDRESS:
6
7 ADDRESSEE: PATENT ADMINISTRATOR/CREATIVE BIOMOLECULES,
8
9 ADDRESSEE: INC.
10
11 STREET: 35 SOUTH STREET
12
13 CITY: HOPKINTON
14
15 STATE: MASS.
16
17 COUNTRY: USA
18
19 ZIP: 01748
20
21 COMPUTER READABLE FORM:
22
23 MEDIUM TYPE: FLOPPY disk
24
25 COMPUTER: IBM PC compatible
26
27 SOFTWARE: GENSTAT, GENSTAT DOS
28
29 SOFTWARE: Patentin Release 11.0, Version 11.25
30
31 CURRENT APPLICATION DATA:
32
33 APPLICATION NUMBER: PCT/US93/07189
34
35 FILING DATE: 19931079

```

1  FEATURE:
2  NAME/REV:  CD5
3  LOCATION:  104...1193
4  OTHER INFORMATION:  /function="ONCOGENIC PROTEIN"
5  OTHER INFORMATION:  /product="MOPI."
6  OTHER INFORMATION:  /note="MOPI (CDNA)."
7
8  PCR-US92-01968-18

```

```

Query Match      0.3% Score 18: 88 4: Length 1873:
Best Local Similarity 100.0% Pred. No. 1.4e+02:
Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0
Qy 385 aatgaataaaaaaaaaa 402
    |||||
Db 1835 AATCAAAAAAAAAAAAA 1852

```

RESULT 148
PCT-US93-05446-8
; Sequence 8, Aff
GENERAL INFO

1 MEDIUM TYPE: Floppy disk
2 COMPUTER: IBM PC compatible
3 OPERATING SYSTEM: PC-DOS/MS-DOS
4 FILE NAME: C:\MSDOS\IBMRN1.Rln Release #1.0, Version #1.25
5 CURRENT FILE SIZE: 1000000
6 APPLICATION NUMBER: PCT/US91/05446
7 FILING DATE: 19920608
8
9 CLASSIFICATION:
10 ATTORNEY INFORMATION:
11 NAME: PITCHER, ESQ., EDWARD R.
12 REGISTRATION NUMBER: 27,829
13 REFERENCE/DOCKET NUMBER: STX-057
14 REGISTRATION/DOCKET INFORMATION:
15 TELEPHONE NO. 1: 202-331-1100
16 INFORMATION FOR SEQ ID NO. 8:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 1873 base pairs

Tue May 27 09:32:18 2001

us-09-410-835-4.011g.rn1

Page 252

```

1 CLASSIFICATION:
2
3 PRIOR APPLICATION DATA:
4
5 PDB accession number:
6
7 FILING DATE:
8
9 ATTORNEY/AGENT INFORMATION:
10
11 NAME: KELLEY, ROBIN D.
12 REGISTRATION NUMBER: 34,637
13 FILING OFFICE: USPTO, NEWARK, NJ, CNP-081CP
14 INFORMATION FOR SEQ ID NO. 3:
15
16 SEQUENCE CHARACTERISTICS:
17
18 LENGTH: 1873 base pairs
19
20 TYPE: nucleic acid
21
22 TOPOLOGY: linear, single
23
24 MOLECULE TYPE: cDNA
25
26 NAME/KEY: CDS
27
28 LOCATION: 104..1193
29
30 OTHER INFORMATION: //function= "ONCOGENIC PROTEIN"
31
32 OTHER INFORMATION: //product= "MOP1"
33
34 OTHER INFORMATION: //note= "MOP1 CDS"
35
36 CDS-00893 01189-3

```

```

Query Match      0.38; Score 18; DB 4; Length 1873;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

PC-05831-0130-18
Sequence 18, Application PC/1059107190
OF
CONTRIBUTOR:
APPLICANT:
TITLE OF INVENTION: MORPHOGEN-ENRICHED DIETARY COMPOSITION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: 10000 UNIVERSITY BLVD., SUITE 100, WILSONVILLE, OR 97154
STREET: 15 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: PDPY d18
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SEQUENCE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US93/07190
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
TELEPHONE: 617/248-7000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
FAX: 617/248-7100
SEQUENCE CHARACTERISTICS: 18:
LENGTH: 1873 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: CDNA
HYPOHETICAL: NO
ANTI-SENSE: NO
ORIGIN: HOPKINTON
ORGANISM: HUMAN
TISSUE TYPE: EMBRIO
FEATURE: CDG 1393
LOCATION: 104, 1393
OTHER INFORMATION: /function="OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product="MOP1"
OTHER INFORMATION: /note="MOP1 (CDNA)"
PCT-US93-07190-18

Query Match 0.3% Score 18; DB 4; Length 1873;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 atgagagagagagagagagag 402
DB 1835 atgagagagagagagagagag 1852

RESULT 151
PCT-US93-07331-18
SEQUENCE: Patent Release #1.0, Version #1.25
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MORPHOGEN-INDUCED NERVE REGENERATION AND
NAMES OF INVENTORS:
ADDRESSER: CREATIVE BIOMOLECULES, INC.
CORRESPONDENCE ADDRESS:
STREET: 35 SOUTH STREET

Tue Mar 27 09:32:18 2001

us-09-410-835-4.01lg.rml

Page 235

PCT-US93-08742-18
SEQUENCE: Patent Release #1.0, Version #1.25
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MORPHOGEN-INDUCED PERIODONTAL TISSUE REGENERATION
NAMES OF INVENTORS:
ADDRESSER: CREATIVE BIOMOLECULES, INC.
CORRESPONDENCE ADDRESS:
STREET: 45 SOUTH STREET
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
COMPUTER TYPE: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: PCT/US93/08742
CLASSIFICATION:
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
TELEPHONE: 617/248-7000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
FAX: 617/248-7100
SEQUENCE CHARACTERISTICS: 18:
LENGTH: 1873 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: CDNA
HYPOHETICAL: NO
ANTI-SENSE: NO
ORIGIN: HOPKINTON
ORGANISM: HUMAN
TISSUE TYPE: EMBRIO
FEATURE: CDG 1393
LOCATION: 104, 1393
OTHER INFORMATION: /function="OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product="MOP1"
OTHER INFORMATION: /note="MOP1 (CDNA)"
PCT-US93-08742-18

Tue Mar 27 09:32:18 2001

us-09-410-835-4.01lg.rml

Page 234

CITY: HOPKINTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
COMPUTER TYPE: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: PCT/US93/07231
CLASSIFICATION:
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
TELEPHONE: 617/248-7000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
FAX: 617/248-7100
SEQUENCE CHARACTERISTICS: 18:
LENGTH: 1873 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: CDNA
HYPOHETICAL: NO
ANTI-SENSE: NO
ORIGIN: HOPKINTON
ORGANISM: HUMAN
TISSUE TYPE: EMBRIO
FEATURE: CDG 1393
LOCATION: 104, 1393
OTHER INFORMATION: /function="OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product="MOP1"
OTHER INFORMATION: /note="MOP1 (CDNA)"
PCT-US93-07231-18

Query Match 0.3% Score 18; DB 4; Length 1873;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 atgagagagagagagagagag 402
DB 1835 atgagagagagagagagagag 1852

RESULT 152

Tue Mar 27 09:32:18 2001

us-09-410-835-4.01lg.rml

Page 236

Query Match 0.3% Score 18; DB 4; Length 1873;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 atgagagagagagagagagag 402
DB 1835 atgagagagagagagagagag 1852

RESULT 153
PCT-US93-08808-18
SEQUENCE: Patent Release #1.0, Version #1.25
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION
NAMES OF INVENTORS:
ADDRESSER: CREATIVE BIOMOLECULES, INC.
CORRESPONDENCE ADDRESS:
STREET: 45 SOUTH STREET
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
COMPUTER TYPE: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: PCT/US93/08808
CLASSIFICATION:
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
TELEPHONE: 617/248-7000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
FAX: 617/248-7100
SEQUENCE CHARACTERISTICS: 18:
LENGTH: 1873 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: CDNA

TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA

Query Match 0.31, Score 18, DB 1, Length 1892;
Beat Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Caps 0;
DB 1861 AATCAAAAAAAAAAAAAA 1878

RESULT 157

US-08-867-970-1
Sequence 1, Application US/08867970
Sequence No. 08452737
GENERAL INFORMATION:
APPLICANT: Olsen, Henrik S.
APPLICANT: Olsen, Timothy
APPLICANT: Adams, Mark D.
TITLE OF INVENTION: Human Oxalyl-CoA Decarboxylase
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDICAL FIELD: 2809.4143
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release 11.0, Version 11.10
CURRENT APPLICATION DATA:
FILING DATE: JUN-3-97
CLASSIFICATION: 538
PRIOR APPLICATION DATA:
PRIORITY NUMBER: US 08/458,120
FILING DATE: JUN-15-95
APPLICATION NUMBER: NO PCT/US94/05561
ATTORNEY DATA:
FILING DATE: 18-MAY-1994
ATTORNEY: Benson, Robert L.
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PFI1901
TELECOMMUNICATION INFORMATION:

Tue Mar 27 09:32:18 2001

us-09-410-835-4.0119.rml

Page 263

NAME: Dolay, Lina A.
REGISTRATION NUMBER: 35,491
REFERENCE/DOCKET NUMBER: 19603/610
TELECOMMUNICATION INFORMATION:
FILING DATE: 17-12-1996
TELEPHONE: (716) 333-1610
TELEFAX: (716) 333-1610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1905 base pairs
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-367-117-7

Query Match 0.31, Score 18, DB 3, Length 1905;
Beat Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Caps 0;

DB 1879 AATCAAAAAAAAAAAAAA 1896

RESULT 159

US-08-900-148-1
Sequence 1, Application US/08900148
Sequence No. 08900148
GENERAL INFORMATION:
APPLICANT: Schroeder, Julian I.
APPLICANT: Antosiewicz, Danuta M.
APPLICANT: Czemuchow, Daniel P.
TITLE OF INVENTION: Nucleic Acid Encoding Metal Uptake
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: University of Maryland and Townsend and Cow LLP
STREET: Two Embareddero Center, Fifth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDICAL FIELD: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release 11.0, Version 11.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,148

Tue Mar 27 09:32:18 2001

us-09-410-835-4.0119.rml

Page 262

TELEPHONE: 301-109-4504
TELEFAX: 301-109-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1892 base pairs
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
STRANDEDNESS: single
NAME/KEY: CDS
LOCATION: 10..1744
US-08-867-970-1

Query Match 0.31, Score 18, DB 2, Length 1892;
Beat Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Caps 0;
DB 1861 AATCAAAAAAAAAAAAAA 1878

RESULT 158

US-08-387-117-7
Sequence 1, Application US/08387117
Sequence No. 01716520
GENERAL INFORMATION:
APPLICANT: Huang, Chiu-shiou
APPLICANT: Webster, Alton
APPLICANT: Anderson, Mary E.
TITLE OF INVENTION: Rat Glutathione Synthetase Gene
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Margaret, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDICAL FIELD: 2809.4143
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release 11.0, Version 11.25
CURRENT APPLICATION DATA:
FILING DATE: 09/08/97.117
CLASSIFICATION: S14
ATTORNEY/AGENT INFORMATION:

Tue Mar 27 09:32:18 2001

us-09-410-835-4.0119.rml

Page 264

FILING DATE: 28-JUL-1997
CLASSIFICATION: B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/022,722
FILING DATE: 28-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Basilio, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 03070-0876006
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA

Query Match 0.31, Score 18, DB 2, Length 1892;
Beat Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Caps 0;
DB 1956 AATCAAAAAAAAAAAAAA 1973

RESULT 160

US-08-300-148-1
Sequence 1, Application US/08300148
Sequence No. 08300148
GENERAL INFORMATION:
APPLICANT: Lipman, Marc E.
APPLICANT: Lipman, Marc E.
TITLE OF INVENTION: Isolated Growth Factors That Bind to the
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS: Lipman, Mark E & Beckert
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.

Db 2486 ATOTANAAAAAAAAAAAA 2503

RESULT 173

US-08-728-626-1

Sequence 1, Application US/08/728/626

Patent No. 5910451

GENERAL INFORMATION:

APPLICANT: Pukuda, Michiko N.

TITLE OF INVENTION: Trophinin and Trophinin-Assisting

INVENTOR: Pukuda, Michiko N.

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESS: Campbell and Florea

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/728/626

FILING DATE: 04-OCT-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/439,818

FILING DATE: 05-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9001

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2524 base pairs

TYPE: nucleic acid

STANDARDS: single

FEATURE:

NAME/KEY: CDS

LOCATION: 28..2275

US-08-728-626-1

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 28..2275

US-08-728-626-1

Query Match

Score 18: DB 2, length 2524;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 ATOTANAAAAAAAAAAAA 402

Db 2486 ATOTANAAAAAAAAAAAA 2503

RESULT 175

US-08-514-014-3

Sequence 1, Application US/08/514/014

Patent No. 6111089

GENERAL INFORMATION:

APPLICANT: Pukuda, Michiko N.

TITLE OF INVENTION: Trophinin-Assisting

INVENTOR: Pukuda, Michiko N.

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESS: Campbell and Florea LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/514/014

FILING DATE: 04-OCT-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/317,572

FILING DATE: 04-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9001

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2524 base pairs

TYPE: nucleic acid

STANDARDS: single

FEATURE:

NAME/KEY: CDS

LOCATION: 28..2275

US-08-514-014-3

Query Match

Score 18: DB 2, length 2524;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 ATOTANAAAAAAAAAAAA 402

Db 2486 ATOTANAAAAAAAAAAAA 2503

RESULT 174

US-08-728-626-1

Sequence 1, Application US/08/728/626

Patent No. 5910451

GENERAL INFORMATION:

APPLICANT: Pukuda, Michiko N.

TITLE OF INVENTION: Trophinin and Trophinin-Assisting

INVENTOR: Pukuda, Michiko N.

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESS: Campbell and Florea

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/728/626

FILING DATE: 04-OCT-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/439,818

FILING DATE: 05-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9001

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2524 base pairs

TYPE: nucleic acid

STANDARDS: single

FEATURE:

NAME/KEY: CDS

LOCATION: 28..2275

US-08-728-626-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9001

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2524 base pairs

TYPE: nucleic acid

STANDARDS: single

FEATURE:

NAME/KEY: CDS

LOCATION: 28..2275

US-08-808-599A-1

Query Match

Score 18: DB 3, length 2524;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 ATOTANAAAAAAAAAAAA 402

Db 2486 ATOTANAAAAAAAAAAAA 2503

RESULT 176

US-08-514-014-3

Sequence 3, Application US/08/514/014

Patent No. 5707829

GENERAL INFORMATION:

APPLICANT: Kelleher, Kerry

TITLE OF INVENTION: Trophinin and Trophinin-Assisting

INVENTOR: Kelleher, Kerry

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESS: Legal Alliance

STREET: 4700 Leggett Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: USA

ZIP: 02142

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/514/014

FILING DATE:

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,774
TELEPHONE: (617) 498-9224
TELEFAX: (617) 498-9224
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2582 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURES: 52..2034
US-08-514-0143

Query Match 0.3% Score 18: DB 3: Length 2582:
Best Local Similarity 100.0%: Pred. No. 14402:
Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
CY 385 atgcagagagagagagagagagag 402
DB 2563 AACGAAAGAGAGAGAGAGAGAGAG 2580

RESULT 117
US-08-514-021-3
Sequence 3: Application US/08033823
Patent No. 5969093
GENERAL INFORMATION:
APPLICANT: MCCORMACK, Kenneth
APPLICANT: MCCORMACK, Kenneth
APPLICANT: MCCORMACK, Kenneth
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: 81 Cambridge Park Drive
STREET: 81 Cambridge Park Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:

CORRESPONDENCE ADDRESS:
ADDRESS: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 08/07/97
CLASSIFICATION: 510
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/617,910
CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: CANOL, M. GRUPE
REGISTRATION NUMBER: 37,141
TELEPHONE: (212) 758-4800
TELEFAX: (212) 758-4800
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 2781
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLLECULE TYPE: CDNA
US-08-178-4778-42

Query Match 0.3% Score 18: DB 3: Length 2781:
Best Local Similarity 100.0%: Pred. No. 14402:
Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
CY 385 atgcagagagagagagagagagag 402
DB 2753 AACGAAAGAGAGAGAGAGAGAGAG 2770

RESULT 119
US-08-747-2218-30
Sequence 30: Application US/08472218
Patent No. 6063610

MEDIUM TYPE: floppy disk
COMPUTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 10-APR-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/514,014
FILING DATE: 11-AUG-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,774
TELEPHONE: (617) 498-9224
TELEFAX: (617) 498-9224
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2582 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURES: 52..2034
US-08-633-823-3

Query Match 0.3% Score 18: DB 3: Length 2582:
Best Local Similarity 100.0%: Pred. No. 14402:
Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
CY 385 atgcagagagagagagagagagag 402
DB 2563 AACGAAAGAGAGAGAGAGAGAGAG 2580

RESULT 118
US-08-178-4778-42
Sequence 42: Application US/08178478
Patent No. 5969093
GENERAL INFORMATION:
APPLICANT: MCCORMACK, Kenneth
APPLICANT: MCCORMACK, Kenneth
APPLICANT: MCCORMACK, Kenneth
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: 81 Cambridge Park Drive
STREET: 81 Cambridge Park Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:

GENERAL INFORMATION:
APPLICANT: Silver, Gary M.
REGISTRATION NUMBER: 37,141
TELEPHONE: (212) 758-4800
TELEFAX: (212) 758-4800
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 2781
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURES: 52..2034
US-08-178-4778-42

Query Match 0.3% Score 18: DB 3: Length 2801:
Best Local Similarity 100.0%: Pred. No. 14402:
Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
CY 4558 aaagagagagagagagagagag 4575
DB 1935 AACGAAAGAGAGAGAGAGAGAGAG 1952

RESULT 180
US-08-747-2218-12/c
Sequence 36, Application US/08/7472218
Patent No. 6063510
GENERAL INFORMATION:
APPLICANT: Silver, Gary M.
INVENTOR: Silver, Gary M.
TITLE OF INVENTION: NOVEL CARBOXYLTERASE NUCLEIC ACID
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESS: Carol Talkington Vester, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,2218
CLASSIFICATION: 6063510 December 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Vester, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: PC-1
TELEPHONE: 970/493-7272
TELEFAX: 970/493-9505
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 2801 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-747-2218-32

Query Match
Best Local Similarity: 100.0%; Pctd No. 1,4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4358 aagaaataacagaaaaa 4375
|||||

Best Local Similarity: 100.0%; Pctd No. 1,4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4358 aagaaataacagaaaaa 4375
Db 1918 AACAAATACGAAAH 1955

RESULT 181
US-08-747-2218-36/c
Sequence 36, Application US/08/7472218
Patent No. 6063510
GENERAL INFORMATION:
APPLICANT: Silver, Gary M.
INVENTOR: Silver, Gary M.
TITLE OF INVENTION: NOVEL CARBOXYLTERASE NUCLEIC ACID
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESS: Carol Talkington Vester, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,2218
CLASSIFICATION: 6063510 December 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Vester, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: PC-1
TELEPHONE: 970/493-7272
TELEFAX: 970/493-9505
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 2836 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-747-2218-26

Query Match
Best Local Similarity: 100.0%; Pctd No. 1,4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4358 aagaaataacagaaaaa 4375
|||||

Db 867 AACAAATACGAAAH 850

RESULT 181
US-08-747-2218-24
Sequence 36, Application US/08/7472218
Patent No. 6063510
GENERAL INFORMATION:
APPLICANT: Silver, Gary M.
INVENTOR: Silver, Gary M.
TITLE OF INVENTION: NOVEL CARBOXYLTERASE NUCLEIC ACID
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESS: Carol Talkington Vester, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,2218
CLASSIFICATION: 6063510 December 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Vester, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: PC-1
TELEPHONE: 970/493-7272
TELEFAX: 970/493-9505
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2836 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-747-2218-24

Query Match
Best Local Similarity: 100.0%; Pctd No. 1,4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4358 aagaaataacagaaaaa 4375
|||||

Query Match
Best Local Similarity: 100.0%; Pctd No. 1,4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4358 aagaaataacagaaaaa 4375
Db 889 AACAAATACGAAAH 882

RESULT 181
US-09-014-969-8
Sequence 36, Application US/09/014969
Patent No. 5965397
GENERAL INFORMATION:
APPLICANT: Jacoby, Kenneth
INVENTOR: Jacoby, Kenneth
TITLE OF INVENTION: NOVEL CARBOXYLTERASE NUCLEIC ACID
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESS: Carol Talkington Vester, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: PC-1
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2999 base pairs

Query Match
Best Local Similarity: 100.0%; Pctd No. 1,4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4358 aagaaataacagaaaaa 4375
Db 889 AACAAATACGAAAH 882

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-014-969-8

Query Match 0.31; Score 18; DB 2; Length 3999;
Best Local Similarity 100.0%; Pred.No. 14402;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 aatgaagaaaaaa 402
DB 3981 aatgaagaaaaaa 2998

RESULT 184
US-08-920-234-1
Sequence 1, Application US/08920234
Patent No. 5312746
GENERAL INFORMATION:
APPLICANT: ELLIS, CATHERINE
APPLICANT: JACSON, JEFFREY
APPLICANT: HAYEN, ROTH
TITLE OF INVENTION: HUMAN DISTINGUISHING METALLOPROTEASE
TITLE OF INVENTION: HUMAN DISTINGUISHING METALLOPROTEASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: HAYEN & PRESTIA
CITY: VALLEY Forge
STATE: PA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
CURRENT APPLICATION NO. FOR WINDOWS Version 2.0
APPLICATION NUMBER: US/08/920,234
FILING DATE: 25-AUG-1997
PRIORITY DATE: 435
PRIORITY NUMBER: 435
PRIORITY DATE: 435
PRIORITY NUMBER: 435
FILING DATE:
ATTOREY/AGENT INFORMATION:
ATTORNEY/AGENT NAME: NULL
REGISTRATION NUMBER: 31,011
REFERENCE/DOCKET NUMBER: CH-70237
TELECOMMUNICATION INFORMATION:

FILING DATE: 10-FEB-1994
APPLICATION NUMBER: 617-720-3500
FILING DATE: 19-OCT-1992
ATTOREY/AGENT INFORMATION:
NAME: JANUO, ARTHUR J.
REFERENCE/DOCKET NUMBER: 29,408
REFERENCE/DOCKET NUMBER: 29,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEPHONE: 617-720-3500
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3443 base pairs
TYPE: nucleic acid
STANDEDNESS: single
MOLECULE TYPE: linear DNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGIN: SOURCE:
ORIGIN: SOURCE: (RABBIT)
US-08-539-654-3

Query Match 0.31; Score 18; DB 1; Length 3443;
Best Local Similarity 100.0%; Pred.No. 14402;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 aatgaagaaaaaa 402
DB 3423 aatgaagaaaaaa 3440

RESULT 186
US-08-920-234-1
Sequence 7, Application US/0851079
Patent No. 5312899
GENERAL INFORMATION:
APPLICANT: ELLIS, CATHERINE
APPLICANT: JACSON, JEFFREY
APPLICANT: HAYEN, ROTH
TITLE OF INVENTION: HUMAN DISTINGUISHING METALLOPROTEASE
TITLE OF INVENTION: HUMAN DISTINGUISHING METALLOPROTEASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FORSTER
CITY: Washington
STATE: DC
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3349 base pairs
TYPE: nucleic acid
STANDEDNESS: single
MOLECULE TYPE: linear
US-08-920-234-1

Query Match 0.31; Score 18; DB 2; Length 3349;
Best Local Similarity 100.0%; Pred.No. 14402;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 aatgaagaaaaaa 402
DB 3279 aatgaagaaaaaa 3296

RESULT 185
US-08-920-234-1
Sequence 3, Application US/08526654
Patent No. 5312844
GENERAL INFORMATION:
APPLICANT: HEDIGER, MATTHIAS
APPLICANT: HEDIGER, MATTHIAS
TITLE OF INVENTION: COMPOSITIONS CORRESPONDING TO A HIGH
TITLE OF INVENTION: AFFINITY GLUTAMATE TRANSPORTER MOLECULE AND METHODS FOR
CORRESPONDENCE ADDRESS:
ADDRESSER: WOLP, GREENFIELD & SACRS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
CURRENT APPLICATION NO. FOR WINDOWS Version 2.0
APPLICATION NUMBER: US/08/529,654
FILING DATE:
CLASSIFICATION: 435
PRIORITY DATE:
PRIORITY NUMBER:
APPLICATION NUMBER: US 08/194,719

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
FILING DATE: US/08/591,079
CLASSIFICATION: 435
ATTOREY/AGENT INFORMATION:
NAME: LANE, GAMES, 33,446
REFERENCE/DOCKET NUMBER: 15661-20017-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1500
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3622 base pairs
TYPE: nucleic acid
STANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ORIGIN: SOURCE:
ORIGIN: SOURCE: Salmonella typhimurium
FEATURES:
NAME/KEY: CDS 575..2356
OTHER INFORMATION: /product="S18P"
US-08-591-079-7

Query Match 0.31; Score 18; DB 2; Length 3622;
Best Local Similarity 100.0%; Pred.No. 14402;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4855 aagatctttaggctt 4872
DB 2490 aagatctttaggctt 2473

RESULT 187
US-08-920-234-1
Sequence 1, Application PC/TUS9600419
GENERAL INFORMATION:
APPLICANT: ALLIANT
APPLICANT: Thomas Cloasek, Axel Ulrich, Blythe
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: MX1 SIGNAL TRANSDUCTION DISORDERS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:

ADDRESSER: Lyon & Lyon
STREET: 613 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA: 18748/103/HOCE
PRIORITY APPLICATION DATA: 18748/103/HOCE
CLASSIFICATION: 536
FILING DATE: January 3, 1995
PRIORITY APPLICATION DATA: including application
PRIORITY APPLICATION DATA: described below:
APPLICATION NUMBER: none
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lyon & Lyon
REGISTRATION NUMBER: 13,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 499-1800
TELEFAX: (213) 555-0440
TELEX: 67-3510
FAX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STANDARDS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic
SEQ ID NO: 1

Query Match 0.31; Score 18; DB 4; Length 4104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 aatgatacttagcgctca 402
DB 3881 aatgatacttagcgctca 3986

RESULT 188
US-08-591-079-9/0
Sequence 18: Application US/08591079
Patent No. 5978899

Tue Mar 27 09:32:18 2001

us-09-410-835-4.0119.rml

Page 299

Db 2458 aatgatacttagcgctca 2441

RESULT 189
US-08-757-439-1/0
Sequence 1: Application US/0875439
Patent No. 7574391
GENERAL INFORMATION:
APPLICANT: BADZIONG, Werner
APPLICANT: HABERMAN, Paul
APPLICANT: MOELLER, Joe Jr
TITLE OF INVENTION: PROMOTER SYSTEM FOR USING THE YEAST ADH II
TITLE OF INVENTION: PROMOTER SYSTEM FOR THE PRODUCTION OF HETEROLOGOUS
TITLE OF INVENTION: PROTEINS IN HIGH YIELDS
CORRESPONDENCE ADDRESSES:
ADDRESSER: Polley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,439
PRIORITY APPLICATION: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA: DE 19544233.4
ATTORNEY/AGENT INFORMATION:
NAME: SANDROCK, Colin G.
REGISTRATION NUMBER: 11,298
REFERENCE/DOCKET NUMBER: 18748/103/HOCE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
FILING DATE: 01-06-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lyon & Lyon
REGISTRATION NUMBER: 13,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 499-1800
TELEFAX: (213) 555-0440
TELEX: 67-3510
FAX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STANDARDS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic
SEQ ID NO: 1

Tue Mar 27 09:32:18 2001

us-09-410-835-4.0119.rml

Page 298

GENERAL INFORMATION:
APPLICANT: Exchlinksky, Arturo
APPLICANT: Chen, Kaling
TITLE OF INVENTION: Apoptosis Induced by Shigella Ipas
TITLE OF INVENTION: Apoptosis Induced by Shigella Ipas
TITLE OF INVENTION: Apoptosis Induced by Shigella Ipas
CORRESPONDENCE ADDRESSES:
ADDRESSER: MORRISON & ROBERTS
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,079
PRIORITY APPLICATION: 530
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lyon & Lyon
REGISTRATION NUMBER: 13,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-1500
TELEX: 67-3510
FAX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STANDARDS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: Salmonella typhi
STRAIN: Ty2
FEATURES:
NAME/KEY: CDS, 2324
LOCATION: 543..2324
ORIGIN: 591-079-9
US-08-591-079-9

Query Match 0.31; Score 18; DB 2; Length 5393;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4855 aatgatacttagcgctca 4872

Tue Mar 27 09:32:18 2001

us-09-410-835-4.0119.rml

Page 100

Query Match 0.31; Score 18; DB 2; Length 8491;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 aatgatacttagcgctca 402
DB 7502 aatgatacttagcgctca 7485

RESULT 190
US-08-724-394A-20
Sequence 20: Application US/0872394A
Patent No. 724394A
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kromal, Gregory S.
APPLICANT: LAUER, Peter M.
APPLICANT: RUDOLPH, David M.
APPLICANT: Tauschman, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587237e1
TITLE OF INVENTION: Sequences and Antibodies Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESSES:
ADDRESSER: TOWNSEND AND CREW LLP
STREET: 200 Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
PRIORITY APPLICATION: 536
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lyon & Lyon
REGISTRATION NUMBER: 13,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 499-1800
TELEFAX: (213) 555-0440
TELEX: 67-3510
FAX: 67-3510
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:

Tue Mar 27 09:12:18 2001

LENGTH: 246240 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: cDNA
 FEATURE: misc.feature
 NAME/KEY: 1..246240
 LOCATION: 1..246240
 OTHER INFORMATION: /note= "HLA-H.COMTIG"

Query Match 0.3% Score 18; DB 2; Length 246240;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 63133 AAAAAAAAAAAATCT 63140

RESULT 191
 US-08-724-394A-21
 Sequence 22, Application US/08724394A
 Patent No. 5872237
 GENERAL INFORMATION:
 APPLICANT: Feder, John N.
 APPLICANT: Kromal, Gregory S.
 APPLICANT: Lauer, Peter M.
 APPLICANT: Mody, Roger K.
 APPLICANT: Thomas, Winston
 APPLICANT: Teuchtmann, Kent
 APPLICANT: Wolff, Roger K.
 TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Not different
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/724,394A
 FILING DATE: 01-OCT-1995
 PRIORITY INFORMATION:
 NAME: Feder, Renee A.
 REGISTRATION NUMBER: 017957-000100
 REFERENCE/DOCKET NUMBER:
 TELEPHONE: 415-576-0300
 TELEFAX: 415-576-0300
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: cDNA
 FEATURE: misc.feature
 NAME/KEY: 1..246240
 LOCATION: 1..246240
 OTHER INFORMATION: /note= "HLA-H.COMTIG"

Tue Mar 27 09:12:18 2001

Tue Mar 27 09:12:18 2001

CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Feder, Renee A. 35,116
 REGISTRATION NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-576-0300
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: cDNA
 FEATURE: misc.feature
 NAME/KEY: 1..246240
 LOCATION: 1..246240
 OTHER INFORMATION: /note= "HLA-H.COMTIG"

Query Match 0.3% Score 18; DB 2; Length 246240;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 63133 AAAAAAAAAAAATCT 63140

RESULT 192
 US-08-724-394A-22
 Sequence 22, Application US/08724394A
 Patent No. 5872237
 GENERAL INFORMATION:
 APPLICANT: Feder, John N.
 APPLICANT: Kromal, Gregory S.
 APPLICANT: Lauer, Peter M.
 APPLICANT: Mody, Roger K.
 APPLICANT: Thomas, Winston
 APPLICANT: Teuchtmann, Kent
 APPLICANT: Wolff, Roger K.
 TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
 CITY: San Francisco
 STATE: CA

Tue Mar 27 09:12:18 2001

COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Not different
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/724,394A
 FILING DATE: 01-OCT-1995
 PRIORITY INFORMATION:
 NAME: Feder, Renee A.
 REGISTRATION NUMBER: 017957-000100
 REFERENCE/DOCKET NUMBER:
 TELEPHONE: 415-576-0300
 TELEFAX: 415-576-0300
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: cDNA
 FEATURE: misc.feature
 NAME/KEY: 1..246240
 LOCATION: 1..246240
 OTHER INFORMATION: /note= "HLA-H.COMTIG"

Query Match 0.3% Score 18; DB 2; Length 246240;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 63133 AAAAAAAAAAAATCT 63140

RESULT 193
 US-08-553-367A-17
 Sequence 17, Application US/0855367A
 Patent No. 5935353
 GENERAL INFORMATION:
 APPLICANT: Theodor, Lance et al.
 TITLE OF INVENTION: CA-20-OXIDASE GENE SEQUENCES (As Amended)
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Henderson, Lind & Pomach, L.L.P.

Tue Mar 27 09:12:18 2001

STREET: 2033 K Street, N.W., Suite 800
 CITY: Washington,
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 OPERATING SYSTEM: IBM compatible
 SOFTWARE: Not different
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/553,367A
 FILING DATE: No. 5935353ember 27, 1995
 PRIORITY INFORMATION:
 NAME: Theodor, Lance
 REGISTRATION NUMBER:
 REFERENCE/DOCKET NUMBER: 49/FDA, 5WZ
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202/721-0200
 TELEFAX: 202/721-0250
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE: misc.feature
 NAME/KEY: NO
 LOCATION: NO
 OTHER INFORMATION: /note= "HLA-H.COMTIG"

Query Match 0.3% Score 17; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2641 GAATCAAAATGCGCA 2657

RESULT 194
 US-08-137-990A-25/C
 Sequence 25, Application US/0813990A

